

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 5, 2004, 16:14:14 ; Search time 5 Seconds  
(without alignments)  
282.548 Million cell updates/sec

Title: US-10-057-890A-7  
Perfect score: 30  
Sequence: 1 HQRVH 5

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Query				Description
Result No.	Score	Match	Length	DB	ID	
1	30	100.0	5	5	ABG32536	Abg32536 Scaffold
2	30	100.0	14	4	AAM97437	Aam97437 Human pep
3	30	100.0	15	5	AAM51635	Aam51635 Human zin
4	30	100.0	15	5	AAM51639	Aam51639 Human act
5	30	100.0	20	6	ABO13540	Abol3540 Arabidops
6	30	100.0	21	6	ABO13174	Abol3174 Mouse zin
7	30	100.0	22	6	ABO13306	Abol3306 Mouse zin
8	30	100.0	23	6	ABO11776	Abol1776 Human zin
9	30	100.0	23	6	ABO11810	Abol1810 Human zin

10	30	100.0	23	6	ABO11822	Abol1822	Human	zin
11	30	100.0	23	6	ABO13276	Abol3276	Mouse	zin
12	30	100.0	23	6	ABO13362	Abol3362	Mouse	zin
13	30	100.0	23	6	ABO11900	Abol1900	Human	zin
14	30	100.0	23	6	ABO12406	Abol2406	Human	zin
15	30	100.0	23	6	ABO12765	Abol2765	Human	zin
16	30	100.0	23	6	ABO12788	Abol2788	Human	zin
17	30	100.0	23	6	ABO13072	Abol3072	Mouse	zin
18	30	100.0	23	6	ABO13149	Abol3149	Mouse	zin
19	30	100.0	23	6	ABO13301	Abol3301	Mouse	zin
20	30	100.0	23	6	ABO13313	Abol3313	Mouse	zin
21	30	100.0	23	6	ABO12415	Abol2415	Human	zin
22	30	100.0	23	6	ABO12522	Abol2522	Human	zin
23	30	100.0	23	6	ABO12758	Abol2758	Human	zin
24	30	100.0	23	6	ABO12761	Abol2761	Human	zin
25	30	100.0	23	6	ABO11963	Abol1963	Human	zin
26	30	100.0	23	6	ABO12786	Abol2786	Human	zin
27	30	100.0	23	6	ABO13147	Abol3147	Mouse	zin
28	30	100.0	23	6	ABO13148	Abol3148	Mouse	zin
29	30	100.0	23	6	ABO13254	Abol3254	Mouse	zin
30	30	100.0	23	6	ABO13297	Abol3297	Mouse	zin
31	30	100.0	23	6	ABO13307	Abol3307	Mouse	zin
32	30	100.0	23	6	ABO13322	Abol3322	Mouse	zin
33	30	100.0	23	6	ABO11775	Abol1775	Human	zin
34	30	100.0	23	6	ABO11883	Abol1883	Human	zin
35	30	100.0	23	6	ABO12574	Abol2574	Human	zin
36	30	100.0	23	6	ABO12744	Abol2744	Human	zin
37	30	100.0	23	6	ABO12796	Abol2796	Human	zin
38	30	100.0	23	6	ABO13028	Abol3028	Mouse	zin
39	30	100.0	23	6	ABO13274	Abol3274	Mouse	zin
40	30	100.0	23	6	ABO12103	Abol2103	Human	zin
41	30	100.0	23	6	ABO12408	Abol2408	Human	zin
42	30	100.0	23	6	ABO12740	Abol2740	Human	zin
43	30	100.0	23	6	ABO12762	Abol2762	Human	zin
44	30	100.0	23	6	ABO12925	Abol2925	Mouse	zin
45	30	100.0	23	6	ABO13312	Abol3312	Mouse	zin

# ALIGNMENTS

## RESULT 1

ABG32536

ID ABG32536 standard; peptide; 5 AA.

XX

AC ABG32536;

XX

DT 15-NOV-2002 (first entry)

XX

DE Scaffold domain peptide #2.

XX

KW Scaffolded protein; CCR5; HIV; human immunodeficiency virus infection;

KW ECD; extracellular domain; metal chelating motif; zinc finger protein;

KW integral membrane protein; soluble loop; intracellular domain; ICD;

KW gene therapy; immunogen; viral infection; scaffold domain; human.

XX

OS Homo sapiens.

XX  
 PN WO200260477-A1.  
 XX  
 PD 08-AUG-2002.  
 XX  
 PF 29-JAN-2002; 2002WO-US002377.  
 XX  
 PR 31-JAN-2001; 2001US-0265782P.  
 PR 31-JAN-2001; 2001US-0265858P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Coleman TA, Mansfield B;  
 XX  
 DR WPI; 2002-643357/69.  
 XX  
 PT Novel scaffolded fusion polypeptide useful for therapeutic purposes or  
 PT for screening molecules that bind/activate/inhibit/modulate the  
 PT polypeptide, comprises a functional polypeptide domain fused to a  
 PT scaffold domain.  
 XX  
 PS Disclosure; Page 16; 64pp; English.  
 XX  
 CC The invention relates to a scaffolded fusion polypeptide comprising a  
 CC functional polypeptide domain fused to a scaffold domain, where the  
 CC functional polypeptide domain corresponds to a soluble loop of an  
 CC integral membrane protein (e.g. human CCR5, a transmembrane receptor  
 CC involved in HIV (human immunodeficiency virus) infection). Also included  
 CC are; (1) a polypeptide comprising a scaffold domain; (2) a nucleic acid  
 CC encoding the fusion polypeptide; (3) a vector cassette for the expression  
 CC of the fusion polypeptide comprising an expression region operably linked  
 CC to a promoter, where the expression region comprises a number of  
 CC cassettes, each of which encodes a module, domain or strand of the fusion  
 CC polypeptide and (4) a host cell comprising the vector or nucleic acid.  
 CC The fusion polypeptide is useful for screening molecules that  
 CC bind/activate/inhibit/modulate the fusion polypeptide, by expressing the  
 CC fusion polypeptide from and identifying a molecule that binds to the  
 CC fusion polypeptide. The fusion polypeptide is useful in diagnostic  
 CC methods, in assays to identify compounds that interact with loops of  
 CC fragments of an extracellular domain (ECD) or an intracellular domain  
 CC (ICD) or to rapidly assay the function of mutated portions of mutant  
 CC integral membrane proteins without having to produce significant  
 CC quantities of the entire mutant integral membrane protein, to generate  
 CC antibodies that recognise the integral membrane proteins from which they  
 CC are designed, to competitively bind the ligand of a naturally occurring  
 CC receptor in vitro or in vivo, to display and/or screen soluble domains  
 CC from protein such as integral membrane proteins, to probe the structure  
 CC of ECD or ICD, or both, of an integral protein membrane, to modulate the  
 CC activity of a receptor in vivo, and for treating or preventing viral  
 CC infection, preferably human HIV infection e.g. by gene therapy using the  
 CC encoding nucleic acid. The present sequence is a scaffold domain suitable  
 CC for inclusion in the fusion protein of the invention  
 XX  
 SQ Sequence 5 AA;

Query Match 100.0%; Score 30; DB 5; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQRVH 5  
 |||||  
 Db 1 HQRVH 5

# RESULT 2

AAM97437

ID AAM97437 standard; peptide; 14 AA.

XX

AC AAM97437;

XX

DT 24-JAN-2002 (first entry)

XX

DE Human peptide #712 encoded by a SNP oligonucleotide.

XX

KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;  
 KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;  
 KW amyloid protein; angiopoietin; apoptosis related protein; cadherin;  
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;  
 KW complement related protein; cytochrome; kinesin; cytokine; interferon;  
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;  
 KW multifactorial disease; autoimmune disease; infection;  
 KW nervous system disease.

XX

OS Homo sapiens.

XX

PN WO200147944-A2.

XX

PD 05-JUL-2001.

XX

PF 28-DEC-2000; 2000WO-US035498.

XX

PR 28-DEC-1999; 99US-0173419P.

PR 27-DEC-2000; 2000US-00173419.

XX

PA (CURA-) CURAGEN CORP.

XX

PI Shimkets RA, Leach M;

XX

DR WPI; 2001-465210/50.

XX

PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,  
 PT oncogenes and histones, useful for diagnosing and treating, e.g. cancer,  
 PT autoimmune diseases and infections.

XX

PS Disclosure; Page 3823; 4143pp; English.

XX

CC The present invention relates to oligonucleotides (see AAL26793-AAL34659)  
 CC encoding polymorphic variants of proteins related to amylases, amyloid  
 CC proteins, angiopoietin, apoptosis related proteins, cadherin, cyclin,  
 CC polymerase, oncogenes, histones, kinases, colony stimulating factors,  
 CC complement related proteins, cytochromes, kinesins, cytokines,  
 CC interferons, interleukins, G-protein coupled receptors and thioesterases.  
 CC The present sequence is a peptide encoded by one such oligonucleotide.  
 CC The oligonucleotides and the peptides encoded by them may be used in the

CC prevention, diagnosis and treatment of diseases associated with  
CC inappropriate expression of the proteins listed above. Disorders that may  
CC be prevented, diagnosed and/or treated include multifactorial diseases  
CC with a genetic component, such as autoimmune diseases (e.g. rheumatoid  
CC arthritis, multiple sclerosis, diabetes, systemic lupus erythromatosus  
CC and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,  
CC brain, breast, colon and kidney, leukaemia), diseases of the nervous  
CC system and an infection of pathogenic organisms  
XX  
SQ Sequence 14 AA;

Query Match 100.0%; Score 30; DB 4; Length 14;  
Best Local Similarity 100.0%; Pred. No. 8;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQRVH 5  
| | | | |  
Db 8 HQRVH 12

RESULT 3

AAM51635

ID AAM51635 standard; peptide; 15 AA.

XX

AC AAM51635;

XX

DT 18-FEB-2002 (first entry)

XX

DE Human zinc finger protein 22 N-terminal peptide.

XX

KW Human; zinc finger protein 22; cancer; nosohaemia; infection; HIV;

KW human immunodeficiency virus; immunological disease;

KW inflammatory disorder.

XX

OS Homo sapiens.

XX

PN CN1307039-A.

XX

PD 08-AUG-2001.

XX

PF 26-JAN-2000; 2000CN-00111545.

XX

PR 26-JAN-2000; 2000CN-00111545.

XX

PA (BODA-) BODAO GENE TECH CO LTD SHANGHAI.

XX

PI Mao Y, Xie Y;

XX

DR WPI; 2002-062741/09.

XX

PT Polypeptide-human zinc finger protein 22 and polynucleotide for coding  
PT said polypeptide.

XX

PS Example 6; Page 19 (disclosure); 34pp; Chinese.

XX

CC The invention relates to a novel polypeptide, human zinc finger protein  
CC 22. The polypeptide is useful for treating various diseases, such as

CC malignant tumours, nosohaemia, HIV infection, immunological diseases and  
CC inflammatory disorder. The present sequence is the N-terminus of the  
CC polypeptide of the invention  
XX  
SQ Sequence 15 AA;

Query Match 100.0%; Score 30; DB 5; Length 15;  
Best Local Similarity 100.0%; Pred. No. 8.6;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQRVH 5  
| | | | |  
Db 3 HQRVH 7

RESULT 4

AAM51639

ID AAM51639 standard; peptide; 15 AA.

XX

AC AAM51639;

XX

DT 18-FEB-2002 (first entry)

XX

DE Human actin 15 N-terminal peptide.

XX

KW Human; zinc finger; PHD finger; actin 15; cancer; nosohaemia; HIV;

KW human immunodeficiency virus; infection; immunological disease;

KW inflammatory disorder.

XX

OS Homo sapiens.

XX

PN CN1307041-A.

XX

PD 08-AUG-2001.

XX

PF 26-JAN-2000; 2000CN-00111549.

XX

PR 26-JAN-2000; 2000CN-00111549.

XX

PA (BODA-) BODAO GENE TECH CO LTD SHANGHAI.

XX

PI Mao Y, Xie Y;

XX

DR WPI; 2002-062743/09.

XX

PT Polypeptide-human zinc finger and PHD finger structural doman-contg actin  
PT 15 and polynucleotide for coding said polypeptide.

XX

PS Example 6; Page 20 (disclosure); 35pp; Chinese.

XX

CC The invention relates to a novel polypeptide, human zinc finger and PHD  
CC finger structural domain-contig actin 15. It is useful in the treatment  
CC of cancer, nosohaemia, HIV infection, immunological diseases and  
CC inflammatory disorders. The present sequence is the N-terminus of the  
CC polypeptide of the invention

XX

SQ Sequence 15 AA;

Query Match 100.0%; Score 30; DB 5; Length 15;  
Best Local Similarity 100.0%; Pred. No. 8.6;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQRVH 5  
|||||  
Db 2 HQRVH 6

RESULT 5

ABO13540

ID ABO13540 standard; peptide; 20 AA.

XX

AC ABO13540;

XX

DT 25-AUG-2003 (first entry)

XX

DE Arabidopsis zinc finger DNA binding domain #13.

XX

KW Composite binding polypeptide; zinc finger nucleic acid binding domain;  
KW autoimmune disorder; immunosuppressive; zinc finger DNA binding domain.

XX

OS Arabidopsis sp.

XX

PN WO200299084-A2.

XX

PD 12-DEC-2002.

XX

PF 04-APR-2002; 2002WO-US022272.

XX

PR 04-APR-2001; 2001GB-00008491.

XX

PA (SANG-) SANGAMO BIOSCIENCES INC.

XX

PI Moore M, Sepp A, Isalan M, Choo Y;

XX

DR WPI; 2003-278214/27.

XX

PT New composite binding zinc finger polypeptide, useful for designing  
PT sequence-specific binding proteins regulating gene expression in the  
PT fields of molecular biology, and for the diagnosis and treatment of  
PT autoimmune disorders.

XX

PS Example 3; Page 111; 157pp; English.

XX

CC The invention relates to a composite binding polypeptide comprising a  
CC first natural binding domain derived from a first natural binding  
CC polypeptide and a second natural binding domain derived from a second  
CC natural binding polypeptide, where the first and second natural binding  
CC polypeptides may be the same or different and where the polypeptide binds  
CC to a target differing from the natural target of both the first and  
CC second binding polypeptides. The invention also relates to a chimeric  
CC polypeptide comprising a binding polypeptide cited above and a biological  
CC effector domain, a library of natural binding domains, a library of  
CC natural zinc finger nucleic acid binding domains comprising a linker  
CC attached to it, a method for selecting a binding polypeptide capable of

CC binding to a target site and a method for designing a composite binding  
CC polypeptide. The methods and compositions of the present invention are  
CC useful for designing sequence-specific binding proteins for regulation of  
CC gene expression in the fields of molecular biology. They can also be used  
CC for the diagnosis and treatment of autoimmune disorders, and as research  
CC tools and in transgenic animals. This sequence represents an Arabidopsis  
CC zinc finger DNA binding domain used in the scope of the invention

XX

SQ Sequence 20 AA;

Query Match 100.0%; Score 30; DB 6; Length 20;

Best Local Similarity 100.0%; Pred. No. 12;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQRVH 5

||||

Db 16 HQRVH 20

#### RESULT 6

ABO13174

ID ABO13174 standard; peptide; 21 AA.

XX

AC ABO13174;

XX

DT 25-AUG-2003 (first entry)

XX

DE Mouse zinc finger DNA binding domain #280.

XX

KW Composite binding polypeptide; zinc finger nucleic acid binding domain;  
KW autoimmune disorder; immunosuppressive; zinc finger DNA binding domain;  
KW mouse.

XX

OS Mus sp.

XX

PN WO200299084-A2.

XX

PD 12-DEC-2002.

XX

PF 04-APR-2002; 2002WO-US022272.

XX

PR 04-APR-2001; 2001GB-00008491.

XX

PA (SANG-) SANGAMO BIOSCIENCES INC.

XX

PI Moore M, Sepp A, Isalan M, Choo Y;

XX

DR WPI; 2003-278214/27.

XX

PT New composite binding zinc finger polypeptide, useful for designing  
PT sequence-specific binding proteins regulating gene expression in the  
PT fields of molecular biology, and for the diagnosis and treatment of  
PT autoimmune disorders.

XX

PS Example 3; Page 103; 157pp; English.

XX

CC The invention relates to a composite binding polypeptide comprising a



CC first natural binding domain derived from a first natural binding  
CC polypeptide and a second natural binding domain derived from a second  
CC natural binding polypeptide, where the first and second natural binding  
CC polypeptides may be the same or different and where the polypeptide binds  
CC to a target differing from the natural target of both the first and  
CC second binding polypeptides. The invention also relates to a chimeric  
CC polypeptide comprising a binding polypeptide cited above and a biological  
CC effector domain, a library of natural binding domains, a library of  
CC natural zinc finger nucleic acid binding domains comprising a linker  
CC attached to it, a method for selecting a binding polypeptide capable of  
CC binding to a target site and a method for designing a composite binding  
CC polypeptide. The methods and compositions of the present invention are  
CC useful for designing sequence-specific binding proteins for regulation of  
CC gene expression in the fields of molecular biology. They can also be used  
CC for the diagnosis and treatment of autoimmune disorders, and as research  
CC tools and in transgenic animals. This sequence represents a mouse zinc  
CC finger DNA binding domain used in the scope of the invention

XX

SQ Sequence 21 AA;

Query Match 100.0%; Score 30; DB 6; Length 21;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQRVH 5  
|||||  
Db 17 HQRVH 21

RESULT 7

AB013306

ID AB013306 standard; peptide; 22 AA.

XX

AC AB013306;

XX

DT 25-AUG-2003 (first entry)

XX

DE Mouse zinc finger DNA binding domain #412.

XX

KW Composite binding polypeptide; zinc finger nucleic acid binding domain;  
KW autoimmune disorder; immunosuppressive; zinc finger DNA binding domain;  
KW mouse.

XX

OS Mus sp.

XX

PN WO200299084-A2.

XX

PD 12-DEC-2002.

XX

PF 04-APR-2002; 2002WO-US022272.

XX

PR 04-APR-2001; 2001GB-00008491.

XX

PA (SANG-) SANGAMO BIOSCIENCES INC.

XX

PI Moore M, Sepp A, Isalan M, Choo Y;

XX

DR WPI; 2003-278214/27.

XX

PT New composite binding zinc finger polypeptide, useful for designing  
PT sequence-specific binding proteins regulating gene expression in the  
PT fields of molecular biology, and for the diagnosis and treatment of  
PT autoimmune disorders.

XX

PS Example 3; Page 106; 157pp; English.

XX

CC The invention relates to a composite binding polypeptide comprising a  
CC first natural binding domain derived from a first natural binding  
CC polypeptide and a second natural binding domain derived from a second  
CC natural binding polypeptide, where the first and second natural binding  
CC polypeptides may be the same or different and where the polypeptide binds  
CC to a target differing from the natural target of both the first and  
CC second binding polypeptides. The invention also relates to a chimeric  
CC polypeptide comprising a binding polypeptide cited above and a biological  
CC effector domain, a library of natural binding domains, a library of  
CC natural zinc finger nucleic acid binding domains comprising a linker  
CC attached to it, a method for selecting a binding polypeptide capable of  
CC binding to a target site and a method for designing a composite binding  
CC polypeptide. The methods and compositions of the present invention are  
CC useful for designing sequence-specific binding proteins for regulation of  
CC gene expression in the fields of molecular biology. They can also be used  
CC for the diagnosis and treatment of autoimmune disorders, and as research  
CC tools and in transgenic animals. This sequence represents a mouse zinc  
CC finger DNA binding domain used in the scope of the invention

XX

SQ Sequence 22 AA;

Query Match 100.0%; Score 30; DB 6; Length 22;

Best Local Similarity 100.0%; Pred. No. 13;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQRVH 5

||||

Db 18 HQRVH 22

RESULT 8

ABO11776

ID ABO11776 standard; peptide; 23 AA.

XX

AC ABO11776;

XX

DT 25-AUG-2003 (first entry)

XX

DE Human zinc finger DNA binding domain #76.

XX

KW Composite binding polypeptide; zinc finger nucleic acid binding domain;  
KW autoimmune disorder; immunosuppressive; zinc finger DNA binding domain;  
KW human.

XX

OS Homo sapiens.

XX

PN WO200299084-A2.

XX

PD 12-DEC-2002.  
 XX  
 PF 04-APR-2002; 2002WO-US022272.  
 XX  
 PR 04-APR-2001; 2001GB-00008491.  
 XX  
 PA (SANG-) SANGAMO BIOSCIENCES INC.  
 XX  
 PI Moore M, Sepp A, Isalan M, Choo Y;  
 XX  
 DR WPI; 2003-278214/27.  
 XX  
 PT New composite binding zinc finger polypeptide, useful for designing  
 PT sequence-specific binding proteins regulating gene expression in the  
 PT fields of molecular biology, and for the diagnosis and treatment of  
 PT autoimmune disorders.  
 XX  
 PS Example 1; Page 71; 157pp; English.  
 XX  
 CC The invention relates to a composite binding polypeptide comprising a  
 CC first natural binding domain derived from a first natural binding  
 CC polypeptide and a second natural binding domain derived from a second  
 CC natural binding polypeptide, where the first and second natural binding  
 CC polypeptides may be the same or different and where the polypeptide binds  
 CC to a target differing from the natural target of both the first and  
 CC second binding polypeptides. The invention also relates to a chimeric  
 CC polypeptide comprising a binding polypeptide cited above and a biological  
 CC effector domain, a library of natural binding domains, a library of  
 CC natural zinc finger nucleic acid binding domains comprising a linker  
 CC attached to it, a method for selecting a binding polypeptide capable of  
 CC binding to a target site and a method for designing a composite binding  
 CC polypeptide. The methods and compositions of the present invention are  
 CC useful for designing sequence-specific binding proteins for regulation of  
 CC gene expression in the fields of molecular biology. They can also be used  
 CC for the diagnosis and treatment of autoimmune disorders, and as research  
 CC tools and in transgenic animals. This sequence represents a human zinc  
 CC finger DNA binding domain used in the scope of the invention  
 XX  
 SQ Sequence 23 AA;

Query Match 100.0%; Score 30; DB 6; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 13;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQRVH 5  
 |||||  
 Db 19 HQRVH 23

RESULT 9  
 AB011810  
 ID AB011810 standard; peptide; 23 AA.  
 XX  
 AC AB011810;  
 XX  
 DT 25-AUG-2003 (first entry)  
 XX

DE Human zinc finger DNA binding domain #110.  
 XX  
 KW Composite binding polypeptide; zinc finger nucleic acid binding domain;  
 KW autoimmune disorder; immunosuppressive; zinc finger DNA binding domain;  
 KW human.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200299084-A2.  
 XX  
 PD 12-DEC-2002.  
 XX  
 PF 04-APR-2002; 2002WO-US022272.  
 XX  
 PR 04-APR-2001; 2001GB-00008491.  
 XX  
 PA (SANG-) SANGAMO BIOSCIENCES INC.  
 XX  
 PI Moore M, Sepp A, Isalan M, Choo Y;  
 XX  
 DR WPI; 2003-278214/27.  
 XX  
 PT New composite binding zinc finger polypeptide, useful for designing  
 PT sequence-specific binding proteins regulating gene expression in the  
 PT fields of molecular biology, and for the diagnosis and treatment of  
 PT autoimmune disorders.  
 XX  
 PS Example 1; Page 72; 157pp; English.  
 XX  
 CC The invention relates to a composite binding polypeptide comprising a  
 CC first natural binding domain derived from a first natural binding  
 CC polypeptide and a second natural binding domain derived from a second  
 CC natural binding polypeptide, where the first and second natural binding  
 CC polypeptides may be the same or different and where the polypeptide binds  
 CC to a target differing from the natural target of both the first and  
 CC second binding polypeptides. The invention also relates to a chimeric  
 CC polypeptide comprising a binding polypeptide cited above and a biological  
 CC effector domain, a library of natural binding domains, a library of  
 CC natural zinc finger nucleic acid binding domains comprising a linker  
 CC attached to it, a method for selecting a binding polypeptide capable of  
 CC binding to a target site and a method for designing a composite binding  
 CC polypeptide. The methods and compositions of the present invention are  
 CC useful for designing sequence-specific binding proteins for regulation of  
 CC gene expression in the fields of molecular biology. They can also be used  
 CC for the diagnosis and treatment of autoimmune disorders, and as research  
 CC tools and in transgenic animals. This sequence represents a human zinc  
 CC finger DNA binding domain used in the scope of the invention  
 XX  
 SQ Sequence 23 AA;

Query Match 100.0%; Score 30; DB 6; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 13;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HQRVH 5  
 |||||  
 Db 19 HQRVH 23

RESULT 10

ABO11822

ID ABO11822 standard; peptide; 23 AA.

XX

AC ABO11822;

XX

DT 25-AUG-2003 (first entry)

XX

DE Human zinc finger DNA binding domain #122.

XX

KW Composite binding polypeptide; zinc finger nucleic acid binding domain;  
KW autoimmune disorder; immunosuppressive; zinc finger DNA binding domain;  
KW human.

XX

OS Homo sapiens.

XX

PN WO200299084-A2.

XX

PD 12-DEC-2002.

XX

PF 04-APR-2002; 2002WO-US022272.

XX

PR 04-APR-2001; 2001GB-00008491.

XX

PA (SANG-) SANGAMO BIOSCIENCES INC.

XX

PI Moore M, Sepp A, Isalan M, Choo Y;

XX

DR WPI; 2003-278214/27.

XX

PT New composite binding zinc finger polypeptide, useful for designing  
PT sequence-specific binding proteins regulating gene expression in the  
PT fields of molecular biology, and for the diagnosis and treatment of  
PT autoimmune disorders.

XX

PS Example 1; Page 72; 157pp; English.

XX

CC The invention relates to a composite binding polypeptide comprising a  
CC first natural binding domain derived from a first natural binding  
CC polypeptide and a second natural binding domain derived from a second  
CC natural binding polypeptide, where the first and second natural binding  
CC polypeptides may be the same or different and where the polypeptide binds  
CC to a target differing from the natural target of both the first and  
CC second binding polypeptides. The invention also relates to a chimeric  
CC polypeptide comprising a binding polypeptide cited above and a biological  
CC effector domain, a library of natural binding domains, a library of  
CC natural zinc finger nucleic acid binding domains comprising a linker  
CC attached to it, a method for selecting a binding polypeptide capable of  
CC binding to a target site and a method for designing a composite binding  
CC polypeptide. The methods and compositions of the present invention are  
CC useful for designing sequence-specific binding proteins for regulation of  
CC gene expression in the fields of molecular biology. They can also be used  
CC for the diagnosis and treatment of autoimmune disorders, and as research  
CC tools and in transgenic animals. This sequence represents a human zinc  
CC finger DNA binding domain used in the scope of the invention

XX

SQ Sequence 23 AA;

Query Match 100.0%; Score 30; DB 6; Length 23;

Best Local Similarity 100.0%; Pred. No. 13;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQRVH 5

|||||

Db 19 HQRVH 23

RESULT 11

ABO13276

ID ABO13276 standard; peptide; 23 AA.

XX

AC ABO13276;

XX

DT 25-AUG-2003 (first entry)

XX

DE Mouse zinc finger DNA binding domain #382.

XX

KW Composite binding polypeptide; zinc finger nucleic acid binding domain;

KW autoimmune disorder; immunosuppressive; zinc finger DNA binding domain;

KW mouse.

XX

OS Mus sp.

XX

PN WO200299084-A2.

XX

PD 12-DEC-2002.

XX

PF 04-APR-2002; 2002WO-US022272.

XX

PR 04-APR-2001; 2001GB-00008491.

XX

PA (SANG-) SANGAMO BIOSCIENCES INC.

XX

PI Moore M, Sepp A, Isalan M, Choo Y;

XX

DR WPI; 2003-278214/27.

XX

PT New composite binding zinc finger polypeptide, useful for designing  
PT sequence-specific binding proteins regulating gene expression in the  
PT fields of molecular biology, and for the diagnosis and treatment of  
PT autoimmune disorders.

XX

PS Example 3; Page 105; 157pp; English.

XX

CC The invention relates to a composite binding polypeptide comprising a  
CC first natural binding domain derived from a first natural binding  
CC polypeptide and a second natural binding domain derived from a second  
CC natural binding polypeptide, where the first and second natural binding  
CC polypeptides may be the same or different and where the polypeptide binds  
CC to a target differing from the natural target of both the first and  
CC second binding polypeptides. The invention also relates to a chimeric  
CC polypeptide comprising a binding polypeptide cited above and a biological

CC effector domain, a library of natural binding domains, a library of  
CC natural zinc finger nucleic acid binding domains comprising a linker  
CC attached to it, a method for selecting a binding polypeptide capable of  
CC binding to a target site and a method for designing a composite binding  
CC polypeptide. The methods and compositions of the present invention are  
CC useful for designing sequence-specific binding proteins for regulation of  
CC gene expression in the fields of molecular biology. They can also be used  
CC for the diagnosis and treatment of autoimmune disorders, and as research  
CC tools and in transgenic animals. This sequence represents a mouse zinc  
CC finger DNA binding domain used in the scope of the invention

XX

SQ Sequence 23 AA;

Query Match 100.0%; Score 30; DB 6; Length 23;

Best Local Similarity 100.0%; Pred. No. 13;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQRVH 5  
| | | | |  
Db 19 HQRVH 23

RESULT 12

ABO13362

ID ABO13362 standard; peptide; 23 AA.

XX

AC ABO13362;

XX

DT 25-AUG-2003 (first entry)

XX

DE Mouse zinc finger DNA binding domain #468.

XX

KW Composite binding polypeptide; zinc finger nucleic acid binding domain;  
KW autoimmune disorder; immunosuppressive; zinc finger DNA binding domain;  
KW mouse.

XX

OS Mus sp.

XX

PN WO200299084-A2.

XX

PD 12-DEC-2002.

XX

PF 04-APR-2002; 2002WO-US022272.

XX

PR 04-APR-2001; 2001GB-00008491.

XX

PA (SANG-) SANGAMO BIOSCIENCES INC.

XX

PI Moore M, Sepp A, Isalan M, Choo Y;

XX

DR WPI; 2003-278214/27.

XX

PT New composite binding zinc finger polypeptide, useful for designing  
PT sequence-specific binding proteins regulating gene expression in the  
PT fields of molecular biology, and for the diagnosis and treatment of  
PT autoimmune disorders.

XX

PS Example 3; Page 107; 157pp; English.

XX

CC The invention relates to a composite binding polypeptide comprising a  
CC first natural binding domain derived from a first natural binding  
CC polypeptide and a second natural binding domain derived from a second  
CC natural binding polypeptide, where the first and second natural binding  
CC polypeptides may be the same or different and where the polypeptide binds  
CC to a target differing from the natural target of both the first and  
CC second binding polypeptides. The invention also relates to a chimeric  
CC polypeptide comprising a binding polypeptide cited above and a biological  
CC effector domain, a library of natural binding domains, a library of  
CC natural zinc finger nucleic acid binding domains comprising a linker  
CC attached to it, a method for selecting a binding polypeptide capable of  
CC binding to a target site and a method for designing a composite binding  
CC polypeptide. The methods and compositions of the present invention are  
CC useful for designing sequence-specific binding proteins for regulation of  
CC gene expression in the fields of molecular biology. They can also be used  
CC for the diagnosis and treatment of autoimmune disorders, and as research  
CC tools and in transgenic animals. This sequence represents a mouse zinc  
CC finger DNA binding domain used in the scope of the invention

XX

SQ Sequence 23 AA;

Query Match 100.0%; Score 30; DB 6; Length 23;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HQRVH 5  
|||||  
Db 19 HQRVH 23

#### RESULT 13

ABO11900

ID ABO11900 standard; peptide; 23 AA.

XX

AC ABO11900;

XX

DT 25-AUG-2003 (first entry)

XX

DE Human zinc finger DNA binding domain #200.

XX

KW Composite binding polypeptide; zinc finger nucleic acid binding domain;  
KW autoimmune disorder; immunosuppressive; zinc finger DNA binding domain;  
KW human.

XX

OS Homo sapiens.

XX

PN WO200299084-A2.

XX

PD 12-DEC-2002.

XX

PF 04-APR-2002; 2002WO-US022272.

XX

PR 04-APR-2001; 2001GB-00008491.

XX

PA (SANG-) SANGAMO BIOSCIENCES INC.



XX  
 PI Moore M, Sepp A, Isalan M, Choo Y;  
 XX  
 DR WPI; 2003-278214/27.  
 XX  
 PT New composite binding zinc finger polypeptide, useful for designing  
 PT sequence-specific binding proteins regulating gene expression in the  
 PT fields of molecular biology, and for the diagnosis and treatment of  
 PT autoimmune disorders.  
 XX  
 PS Example 1; Page 74; 157pp; English.  
 XX  
 CC The invention relates to a composite binding polypeptide comprising a  
 CC first natural binding domain derived from a first natural binding  
 CC polypeptide and a second natural binding domain derived from a second  
 CC natural binding polypeptide, where the first and second natural binding  
 CC polypeptides may be the same or different and where the polypeptide binds  
 CC to a target differing from the natural target of both the first and  
 CC second binding polypeptides. The invention also relates to a chimeric  
 CC polypeptide comprising a binding polypeptide cited above and a biological  
 CC effector domain, a library of natural binding domains, a library of  
 CC natural zinc finger nucleic acid binding domains comprising a linker  
 CC attached to it, a method for selecting a binding polypeptide capable of  
 CC binding to a target site and a method for designing a composite binding  
 CC polypeptide. The methods and compositions of the present invention are  
 CC useful for designing sequence-specific binding proteins for regulation of  
 CC gene expression in the fields of molecular biology. They can also be used  
 CC for the diagnosis and treatment of autoimmune disorders, and as research  
 CC tools and in transgenic animals. This sequence represents a human zinc  
 CC finger DNA binding domain used in the scope of the invention  
 XX  
 SQ Sequence 23 AA;

Query Match 100.0%; Score 30; DB 6; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 13;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQRVH 5  
 |||||  
 Db 19 HQRVH 23

#### RESULT 14

AB012406

ID AB012406 standard; peptide; 23 AA.

XX

AC AB012406;

XX

DT 25-AUG-2003 (first entry)

XX

DE Human zinc finger DNA binding domain #705.

XX

KW Composite binding polypeptide; zinc finger nucleic acid binding domain;  
 KW autoimmune disorder; immunosuppressive; zinc finger DNA binding domain;  
 KW human.

XX

OS Homo sapiens.

XX  
 PN WO200299084-A2.  
 XX  
 PD 12-DEC-2002.  
 XX  
 PF 04-APR-2002; 2002WO-US022272.  
 XX  
 PR 04-APR-2001; 2001GB-00008491.  
 XX  
 PA (SANG-) SANGAMO BIOSCIENCES INC.  
 XX  
 PI Moore M, Sepp A, Isalan M, Choo Y;  
 XX  
 DR WPI; 2003-278214/27.  
 XX  
 PT New composite binding zinc finger polypeptide, useful for designing  
 PT sequence-specific binding proteins regulating gene expression in the  
 PT fields of molecular biology, and for the diagnosis and treatment of  
 PT autoimmune disorders.  
 XX  
 PS Example 2; Page 86; 157pp; English.  
 XX  
 CC The invention relates to a composite binding polypeptide comprising a  
 CC first natural binding domain derived from a first natural binding  
 CC polypeptide and a second natural binding domain derived from a second  
 CC natural binding polypeptide, where the first and second natural binding  
 CC polypeptides may be the same or different and where the polypeptide binds  
 CC to a target differing from the natural target of both the first and  
 CC second binding polypeptides. The invention also relates to a chimeric  
 CC polypeptide comprising a binding polypeptide cited above and a biological  
 CC effector domain, a library of natural binding domains, a library of  
 CC natural zinc finger nucleic acid binding domains comprising a linker  
 CC attached to it, a method for selecting a binding polypeptide capable of  
 CC binding to a target site and a method for designing a composite binding  
 CC polypeptide. The methods and compositions of the present invention are  
 CC useful for designing sequence-specific binding proteins for regulation of  
 CC gene expression in the fields of molecular biology. They can also be used  
 CC for the diagnosis and treatment of autoimmune disorders, and as research  
 CC tools and in transgenic animals. This sequence represents a human zinc  
 CC finger DNA binding domain used in the scope of the invention  
 XX  
 SQ Sequence 23 AA;

Query Match 100.0%; Score 30; DB 6; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 13;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQRVH 5  
 |||||  
 Db 19 HQRVH 23

RESULT 15  
 AB012765  
 ID AB012765 standard; peptide; 23 AA.  
 XX  
 AC AB012765;

XX  
 DT 25-AUG-2003 (first entry)  
 XX  
 DE Human zinc finger DNA binding domain #1064.  
 XX  
 KW Composite binding polypeptide; zinc finger nucleic acid binding domain;  
 KW autoimmune disorder; immunosuppressive; zinc finger DNA binding domain;  
 KW human.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200299084-A2.  
 XX  
 PD 12-DEC-2002.  
 XX  
 PF 04-APR-2002; 2002WO-US022272.  
 XX  
 PR 04-APR-2001; 2001GB-00008491.  
 XX  
 PA (SANG-) SANGAMO BIOSCIENCES INC.  
 XX  
 PI Moore M, Sepp A, Isalan M, Choo Y;  
 XX  
 DR WPI; 2003-278214/27.  
 XX  
 PT New composite binding zinc finger polypeptide, useful for designing  
 PT sequence-specific binding proteins regulating gene expression in the  
 PT fields of molecular biology, and for the diagnosis and treatment of  
 PT autoimmune disorders.  
 XX  
 PS Example 2; Page 93; 157pp; English.  
 XX  
 CC The invention relates to a composite binding polypeptide comprising a  
 CC first natural binding domain derived from a first natural binding  
 CC polypeptide and a second natural binding domain derived from a second  
 CC natural binding polypeptide, where the first and second natural binding  
 CC polypeptides may be the same or different and where the polypeptide binds  
 CC to a target differing from the natural target of both the first and  
 CC second binding polypeptides. The invention also relates to a chimeric  
 CC polypeptide comprising a binding polypeptide cited above and a biological  
 CC effector domain, a library of natural binding domains, a library of  
 CC natural zinc finger nucleic acid binding domains comprising a linker  
 CC attached to it, a method for selecting a binding polypeptide capable of  
 CC binding to a target site and a method for designing a composite binding  
 CC polypeptide. The methods and compositions of the present invention are  
 CC useful for designing sequence-specific binding proteins for regulation of  
 CC gene expression in the fields of molecular biology. They can also be used  
 CC for the diagnosis and treatment of autoimmune disorders, and as research  
 CC tools and in transgenic animals. This sequence represents a human zinc  
 CC finger DNA binding domain used in the scope of the invention  
 XX  
 SQ Sequence 23 AA;  
  
 Query Match 100.0%; Score 30; DB 6; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 13;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy            1 HQRVH 5  
              |||||  
Db            19 HQRVH 23

Search completed: March 5, 2004, 16:22:45  
Job time : 6 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 5, 2004, 16:17:14 ; Search time 1.34259 Seconds  
(without alignments)  
192.262 Million cell updates/sec

Title: US-10-057-890A-7  
Perfect score: 30  
Sequence: 1 HQRVH 5

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents\_AA:\*  
1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	30	100.0	25	3	US-09-253-396A-216	Sequence 216, App
2	30	100.0	26	2	US-08-620-151-55	Sequence 55, Appl
3	30	100.0	149	2	US-08-606-143-24	Sequence 24, Appl
4	30	100.0	150	2	US-08-606-143-26	Sequence 26, Appl
5	30	100.0	150	2	US-08-606-143-29	Sequence 29, Appl
6	30	100.0	217	3	US-09-058-489-48	Sequence 48, Appl
7	30	100.0	288	5	PCT-US95-04801-7	Sequence 7, Appli
8	30	100.0	313	4	US-09-800-729-196	Sequence 196, App
9	30	100.0	315	1	US-08-253-155A-34	Sequence 34, Appl
10	30	100.0	326	4	US-09-800-729-195	Sequence 195, App
11	30	100.0	338	2	US-08-933-750C-4	Sequence 4, Appli

12	30	100.0	338	3	US-09-234-613-4	Sequence 4, Appli
13	30	100.0	368	2	US-08-933-750C-14	Sequence 14, Appl
14	30	100.0	368	3	US-09-234-613-14	Sequence 14, Appl
15	30	100.0	400	4	US-09-252-991A-25966	Sequence 25966, A
16	30	100.0	462	4	US-09-252-991A-20410	Sequence 20410, A
17	30	100.0	488	2	US-08-933-750C-17	Sequence 17, Appl
18	30	100.0	488	3	US-09-234-613-17	Sequence 17, Appl
19	30	100.0	543	4	US-09-362-123A-4	Sequence 4, Appli
20	30	100.0	606	4	US-09-540-236-2752	Sequence 2752, Ap
21	30	100.0	675	1	US-08-317-522A-9	Sequence 9, Appli
22	30	100.0	675	1	US-08-439-818A-9	Sequence 9, Appli
23	30	100.0	675	2	US-08-751-965-9	Sequence 9, Appli
24	30	100.0	675	2	US-08-738-975-9	Sequence 9, Appli
25	30	100.0	675	2	US-08-728-626-9	Sequence 9, Appli
26	30	100.0	675	3	US-08-808-599A-9	Sequence 9, Appli
27	30	100.0	717	4	US-09-881-578A-2	Sequence 2, Appli
28	30	100.0	927	4	US-09-252-991A-16765	Sequence 16765, A
29	30	100.0	1127	4	US-09-252-991A-26849	Sequence 26849, A
30	29	96.7	23	3	US-09-253-396A-218	Sequence 218, App
31	29	96.7	26	2	US-08-620-151-37	Sequence 37, Appl
32	29	96.7	26	2	US-08-620-151-44	Sequence 44, Appl
33	29	96.7	26	2	US-08-620-151-51	Sequence 51, Appl
34	29	96.7	26	2	US-08-620-151-52	Sequence 52, Appl
35	29	96.7	26	2	US-08-620-151-58	Sequence 58, Appl
36	29	96.7	26	2	US-08-620-151-84	Sequence 84, Appl
37	29	96.7	26	2	US-08-620-151-86	Sequence 86, Appl
38	29	96.7	26	2	US-08-620-151-90	Sequence 90, Appl
39	29	96.7	26	2	US-08-620-151-97	Sequence 97, Appl
40	29	96.7	28	1	US-08-331-394-20	Sequence 20, Appl
41	29	96.7	28	1	US-08-250-858-20	Sequence 20, Appl
42	29	96.7	28	1	US-08-446-915-20	Sequence 20, Appl
43	29	96.7	28	2	US-08-744-139-20	Sequence 20, Appl
44	29	96.7	28	3	US-09-253-396A-225	Sequence 225, App
45	29	96.7	28	4	US-08-779-599-20	Sequence 20, Appl

#### ALIGNMENTS

##### RESULT 1

US-09-253-396A-216

; Sequence 216, Application US/09253396A

; Patent No. 6205404

; GENERAL INFORMATION:

; APPLICANT: Genome Dynamics, Inc.

; TITLE OF INVENTION: DNA-Binding Proteins of the Zinc-Finger Class

; FILE REFERENCE: 1116242-0003 file: genome03F.app

; CURRENT APPLICATION NUMBER: US/09/253,396A

; CURRENT FILING DATE: 1999-02-19

; NUMBER OF SEQ ID NOS: 231

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 216

; LENGTH: 25

; TYPE: PRT

; ORGANISM: Xenopus laevis

US-09-253-396A-216

Query Match 100.0%; Score 30; DB 3; Length 25;  
Best Local Similarity 100.0%; Pred. No. 6.2;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQRVH 5  
|||||  
Db 19 HQRVH 23

RESULT 2

US-08-620-151-55

; Sequence 55, Application US/08620151

; Patent No. 5928955

; GENERAL INFORMATION:

; APPLICANT: Imperiali, Barbara

; APPLICANT: Walkup, Grant K.

; TITLE OF INVENTION: PEPTIDYL FLUORESCENT CHEMOSENSOR FOR

; TITLE OF INVENTION: DIVALENT ZINC

; NUMBER OF SEQUENCES: 136

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BRINKS, HOFER, GILSON & LIONE

; STREET: NBC Tower - Suite 3600, 455 N. Cityfront

; STREET: Plaza Drive

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60611-5599

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/620,151

; FILING DATE: 22-MAR-1996

; CLASSIFICATION: 422

; ATTORNEY/AGENT INFORMATION:

; NAME: Shannon, Karen L.

; REGISTRATION NUMBER: 36,675

; REFERENCE/DOCKET NUMBER: 8597/6

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 312-321-4200

; TELEFAX: 312-321-4299

; INFORMATION FOR SEQ ID NO: 55:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 26 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-620-151-55

Query Match 100.0%; Score 30; DB 2; Length 26;

Best Local Similarity 100.0%; Pred. No. 6.4;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQRVH 5

Db                   |||||  
                    20 HQRVH 24

RESULT 3

US-08-606-143-24  
; Sequence 24, Application US/08606143  
; Patent No. 5856155  
; GENERAL INFORMATION:  
; APPLICANT: Li, Min  
; TITLE OF INVENTION: COMPOUNDS AND RELATED METHODS FOR  
; TITLE OF INVENTION: MODULATING POTASSIUM ION CHANNELS AND ASSAYS FOR SUCH  
; TITLE OF INVENTION: COMPOUNDS  
; NUMBER OF SEQUENCES: 45  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Leydig, Voit & Mayer, Ltd.  
; STREET: Two Prudential Plaza, Suite 4900  
; CITY: Chicago  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/606,143  
; FILING DATE: 23-FEB-1996  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kilyk Jr., John  
; REGISTRATION NUMBER: 30763  
; REFERENCE/DOCKET NUMBER: 71756  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 616-5600  
; TELEFAX: (312) 616-5700  
; TELEX: 25-3533  
; INFORMATION FOR SEQ ID NO: 24:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 149 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-606-143-24

Query Match                   100.0%; Score 30; DB 2; Length 149;  
Best Local Similarity       100.0%; Pred. No. 34;  
Matches       5; Conservative   0; Mismatches   0; Indels       0; Gaps       0;

Qy           1 HQRVH 5  
             |||||  
Db           1 HQRVH 5

RESULT 4



US-08-606-143-26  
; Sequence 26, Application US/08606143  
; Patent No. 5856155  
; GENERAL INFORMATION:  
; APPLICANT: Li, Min  
; TITLE OF INVENTION: COMPOUNDS AND RELATED METHODS FOR  
; TITLE OF INVENTION: MODULATING POTASSIUM ION CHANNELS AND ASSAYS FOR SUCH  
; TITLE OF INVENTION: COMPOUNDS  
; NUMBER OF SEQUENCES: 45  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Leydig, Voit & Mayer, Ltd.  
; STREET: Two Prudential Plaza, Suite 4900  
; CITY: Chicago  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/606,143  
; FILING DATE: 23-FEB-1996  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kilyk Jr., John  
; REGISTRATION NUMBER: 30763  
; REFERENCE/DOCKET NUMBER: 71756  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 616-5600  
; TELEFAX: (312) 616-5700  
; TELEX: 25-3533  
; INFORMATION FOR SEQ ID NO: 26:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 150 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-606-143-26

Query Match 100.0%; Score 30; DB 2; Length 150;  
Best Local Similarity 100.0%; Pred. No. 35;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQRVH 5  
|||||  
Db 1 HQRVH 5

RESULT 5  
US-08-606-143-29  
; Sequence 29, Application US/08606143  
; Patent No. 5856155  
; GENERAL INFORMATION:  
; APPLICANT: Li, Min

```

; TITLE OF INVENTION: COMPOUNDS AND RELATED METHODS FOR
; TITLE OF INVENTION: MODULATING POTASSIUM ION CHANNELS AND ASSAYS FOR SUCH
; TITLE OF INVENTION: COMPOUNDS
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Voit & Mayer, Ltd.
; STREET: Two Prudential Plaza, Suite 4900
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/606,143
; FILING DATE: 23-FEB-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kilyk Jr., John
; REGISTRATION NUMBER: 30763
; REFERENCE/DOCKET NUMBER: 71756
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 616-5600
; TELEFAX: (312) 616-5700
; TELEX: 25-3533
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 150 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-606-143-29

```

```

Query Match          100.0%; Score 30; DB 2; Length 150;
Best Local Similarity 100.0%; Pred. No. 35;
Matches      5; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      1 HQRVH 5
        |||||
Db      1 HQRVH 5

```

# RESULT 6

```

US-09-058-489-48
; Sequence 48, Application US/09058489
; Patent No. 6103886
; GENERAL INFORMATION:
; APPLICANT: Whitehead Institute for Biomedical Research
; APPLICANT: Lahn, Bruce
; APPLICANT: Page, David
; TITLE OF INVENTION: Genes in the No. 6103886-Recombining Region of
; TITLE OF INVENTION: the Y Chromosome
; FILE REFERENCE: WHI97-08pA

```

; CURRENT APPLICATION NUMBER: US/09/058,489  
; CURRENT FILING DATE: 1998-04-10  
; EARLIER APPLICATION NUMBER: 60/041,877  
; EARLIER FILING DATE: 1997-04-11  
; NUMBER OF SEQ ID NOS: 91  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 48  
; LENGTH: 217  
; TYPE: PRT  
; ORGANISM: Human  
US-09-058-489-48

Query Match 100.0%; Score 30; DB 3; Length 217;  
Best Local Similarity 100.0%; Pred. No. 49;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQRVH 5  
|||||  
Db 109 HQRVH 113

RESULT 7

PCT-US95-04801-7

; Sequence 7, Application PC/TUS9504801

; GENERAL INFORMATION:

; APPLICANT: Martin, Juan F.  
; APPLICANT: Coque, Juan R.  
; APPLICANT: Enguita, Francisco J.  
; APPLICANT: Fuente, Juan L.  
; APPLICANT: Llarena, Francisco J.  
; APPLICANT: Liras, Paloma  
; TITLE OF INVENTION: DNA ENCODING CEPHAMYCIN BIOSYNTHESIS  
; TITLE OF INVENTION: LATE GENES  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: John W. Wallen III  
; STREET: P.O. Box 2000  
; CITY: Rahway  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07065

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/04801  
; FILING DATE:  
; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Wallen III, John W.  
; REGISTRATION NUMBER: 35,403  
; REFERENCE/DOCKET NUMBER: 19179

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (908) 594-3905  
; TELEFAX: (908) 594-4720

; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 288 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
PCT-US95-04801-7

Query Match 100.0%; Score 30; DB 5; Length 288;  
Best Local Similarity 100.0%; Pred. No. 65;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQRVH 5  
|||||  
Db 128 HQRVH 132

RESULT 8

US-09-800-729-196  
; Sequence 196, Application US/09800729  
; Patent No. 6605592  
; GENERAL INFORMATION:  
; APPLICANT: Ni et al.  
; TITLE OF INVENTION: 32 Human secreted proteins  
; FILE REFERENCE: PZ044P1  
; CURRENT APPLICATION NUMBER: US/09/800,729  
; CURRENT FILING DATE: 2001-03-08  
; PRIOR APPLICATION NUMBER: PCT/US00/26013  
; PRIOR FILING DATE: 2000-09-22  
; PRIOR APPLICATION NUMBER: 60/155,709  
; PRIOR FILING DATE: 1999-09-24  
; NUMBER OF SEQ ID NOS: 217  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 196  
; LENGTH: 313  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-800-729-196

Query Match 100.0%; Score 30; DB 4; Length 313;  
Best Local Similarity 100.0%; Pred. No. 70;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQRVH 5  
|||||  
Db 226 HQRVH 230

RESULT 9

US-08-253-155A-34  
; Sequence 34, Application US/08253155A  
; Patent No. 5691147  
; GENERAL INFORMATION:  
; APPLICANT: Gyuris, Jeno  
; APPLICANT: Draetta, Giulio  
; TITLE OF INVENTION: CDK4 Binding Proteins

```

;   NUMBER OF SEQUENCES:  95
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE:  LAHIVE & COCKFIELD
;   STREET:  60 State Street
;   CITY:  Boston
;   STATE:  MA
;   COUNTRY:  USA
;   ZIP:  02109
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE:  Floppy disk
;   COMPUTER:  IBM PC compatible
;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  ASCII(text)
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/253,155A
;   FILING DATE:  02-JUN-1994
;   CLASSIFICATION:  435
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  Vincent, Matthew P.
;   REGISTRATION NUMBER:  36,709
;   REFERENCE/DOCKET NUMBER:  MII-028
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  (617) 227-7400
;   TELEFAX:  (617) 227-5941
;   INFORMATION FOR SEQ ID NO:  34:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  315 amino acids
;   TYPE:  amino acid
;   TOPOLOGY:  linear
;   MOLECULE TYPE:  peptide
;   FRAGMENT TYPE:  internal
US-08-253-155A-34

```

```

Query Match          100.0%;  Score 30;  DB 1;  Length 315;
Best Local Similarity 100.0%;  Pred. No. 71;
Matches      5;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

```

Qy      1 HQRVH 5
        |||||
Db      32 HQRVH 36

```

```

RESULT 10
US-09-800-729-195
; Sequence 195, Application US/09800729
; Patent No. 6605592
; GENERAL INFORMATION:
; APPLICANT:  Ni et al.
; TITLE OF INVENTION:  32 Human secreted proteins
; FILE REFERENCE:  PZ044P1
; CURRENT APPLICATION NUMBER:  US/09/800,729
; CURRENT FILING DATE:  2001-03-08
; PRIOR APPLICATION NUMBER:  PCT/US00/26013
; PRIOR FILING DATE:  2000-09-22
; PRIOR APPLICATION NUMBER:  60/155,709
; PRIOR FILING DATE:  1999-09-24
; NUMBER OF SEQ ID NOS:  217

```

; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 195  
; LENGTH: 326  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-800-729-195

Query Match 100.0%; Score 30; DB 4; Length 326;  
Best Local Similarity 100.0%; Pred. No. 73;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQRVH 5  
|||||  
Db 239 HQRVH 243

RESULT 11

US-08-933-750C-4

; Sequence 4, Application US/08933750C  
; Patent No. 5932442  
; GENERAL INFORMATION:  
; APPLICANT: Lal, Preeti  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Bandman, Olga  
; APPLICANT: Shah, Purvi  
; APPLICANT: Au-Young, Janice  
; APPLICANT: Yue, Henry  
; APPLICANT: Guegler, Karl J.  
; APPLICANT: Corley, Neil C.  
; TITLE OF INVENTION: HUMAN REGULATORY MOLECULES  
; NUMBER OF SEQUENCES: 98  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/933,750C  
; FILING DATE: September 23, 1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0356 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-845-4166

; TELEX:  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 338 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: HMC1NOT01  
; CLONE: 9337  
US-08-933-750C-4

Query Match 100.0%; Score 30; DB 2; Length 338;  
Best Local Similarity 100.0%; Pred. No. 76;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQRVH 5  
| | | | |  
Db 238 HQRVH 242

RESULT 12

US-09-234-613-4

; Sequence 4, Application US/09234613  
; Patent No. 6132973  
; GENERAL INFORMATION:  
; APPLICANT: Lal, Preeti  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Bandman, Olga  
; APPLICANT: Shah, Purvi  
; APPLICANT: Au-Young, Janice  
; APPLICANT: Yue, Henry  
; APPLICANT: Guegler, Karl J.  
; APPLICANT: Corley, Neil C.  
; TITLE OF INVENTION: HUMAN REGULATORY MOLECULES  
; NUMBER OF SEQUENCES: 98  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/234,613  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/933,750  
; FILING DATE: September 23, 1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.

; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0356 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-845-4166  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 338 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: HMC1NOT01  
; CLONE: 9337  
US-09-234-613-4

Query Match 100.0%; Score 30; DB 3; Length 338;  
Best Local Similarity 100.0%; Pred. No. 76;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQRVH 5  
|||||  
Db 238 HQRVH 242

RESULT 13

US-08-933-750C-14

; Sequence 14, Application US/08933750C  
; Patent No. 5932442  
; GENERAL INFORMATION:  
; APPLICANT: Lal, Preeti  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Bandman, Olga  
; APPLICANT: Shah, Purvi  
; APPLICANT: Au-Young, Janice  
; APPLICANT: Yue, Henry  
; APPLICANT: Guegler, Karl J.  
; APPLICANT: Corley, Neil C.  
; TITLE OF INVENTION: HUMAN REGULATORY MOLECULES  
; NUMBER OF SEQUENCES: 98  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/933,750C  
; FILING DATE: September 23, 1997  
; CLASSIFICATION: 536



```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0356 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 368 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: MMLR3DT01
; CLONE: 569710
US-08-933-750C-14

```

```

Query Match          100.0%; Score 30; DB 2; Length 368;
Best Local Similarity 100.0%; Pred. No. 82;
Matches      5; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      1 HQRVH 5
        |||||
Db      297 HQRVH 301

```

# RESULT 14

US-09-234-613-14

```

; Sequence 14, Application US/09234613
; Patent No. 6132973
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Bandman, Olga
; APPLICANT: Shah, Purvi
; APPLICANT: Au-Young, Janice
; APPLICANT: Yue, Henry
; APPLICANT: Guegler, Karl J.
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
; NUMBER OF SEQUENCES: 98
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS

```

```

; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/234,613
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/933,750
; FILING DATE: September 23, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0356 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 368 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: MMLR3DT01
; CLONE: 569710
US-09-234-613-14

```

```

Query Match          100.0%; Score 30; DB 3; Length 368;
Best Local Similarity 100.0%; Pred. No. 82;
Matches      5; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy          1 HQRVH 5
            |||||
Db          297 HQRVH 301

```

```

RESULT 15
US-09-252-991A-25966
; Sequence 25966, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 25966
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa

```

US-09-252-991A-25966

Query Match 100.0%; Score 30; DB 4; Length 400;  
Best Local Similarity 100.0%; Pred. No. 89;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQRVH 5  
|||||  
Db 192 HQRVH 196

Search completed: March 5, 2004, 16:30:35  
Job time : 1.34259 secs

OM protein - protein search, using sw model

Run on: March 5, 2004, 16:16:19 ; Search time 1.14198 Seconds  
(without alignments)  
421.163 Million cell updates/sec

Title: US-10-057-890A-7  
Perfect score: 30  
Sequence: 1 HQRVH 5

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_78:\*  
1: pirl:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	30	100.0	39	2	D40984	finger protein zfa
2	30	100.0	56	2	S10398	finger protein kox
3	30	100.0	56	2	I37960	zinc finger protei
4	30	100.0	56	2	I37963	zinc finger protei
5	30	100.0	56	2	I37966	zinc finger protei
6	30	100.0	66	2	S47065	finger protein HZF
7	30	100.0	85	2	A42825	Kruppel-type zinc
8	30	100.0	87	2	I38941	zinc finger protei
9	30	100.0	88	2	D43284	finger protein ZNF
10	30	100.0	105	2	B48827	zinc finger protei
11	30	100.0	106	2	D31201	GLI-related finger
12	30	100.0	106	2	T34560	hypothetical prote
13	30	100.0	137	1	QQBED9	HHLF3 protein - hu

14	30	100.0	139	2	I38620	zinc finger protei
15	30	100.0	169	2	A39240	finger protein mfg
16	30	100.0	172	2	S06575	finger protein (cl
17	30	100.0	183	2	S70007	finger protein zfo
18	30	100.0	194	2	I53859	zinc finger protei
19	30	100.0	196	2	S06558	finger protein (cl
20	30	100.0	201	2	I57505	zinc finger protei
21	30	100.0	209	2	S47068	finger protein HZF
22	30	100.0	216	2	S06781	finger protein (cl
23	30	100.0	223	2	S06576	finger protein (cl
24	30	100.0	223	2	S33991	finger protein ZNF
25	30	100.0	223	2	F31201	GLI-related finger
26	30	100.0	247	2	S06553	finger protein (cl
27	30	100.0	258	2	T34601	hypothetical prote
28	30	100.0	261	2	S70006	finger protein zfo
29	30	100.0	288	2	C56281	7alpha-cephem-meth
30	30	100.0	348	2	I38599	zinc finger protei
31	30	100.0	378	2	S33994	finger protein ZNF
32	30	100.0	386	2	T12527	hypothetical prote
33	30	100.0	393	2	JN0533	finger protein pML
34	30	100.0	401	2	A42177	KRAB-domain-contai
35	30	100.0	405	2	D70529	hypothetical prote
36	30	100.0	411	2	S10245	finger protein, te
37	30	100.0	420	2	S65084	finger protein XFG
38	30	100.0	421	2	AE2473	hypothetical prote
39	30	100.0	445	2	S32036	finger protein XFG
40	30	100.0	462	2	I51699	gene XGF 5.1C prot
41	30	100.0	475	2	S03679	finger protein (cl
42	30	100.0	482	2	S18210	hypothetical prote
43	30	100.0	485	2	A40751	finger protein MZF
44	30	100.0	518	1	FWOAG1	12S seed storage g
45	30	100.0	518	2	A36433	globulin precursor

# ALIGNMENTS

## RESULT 1

D40984

finger protein zfas8 - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 28-May-1992 #sequence\_revision 28-May-1992 #text\_change 08-Dec-2000

C;Accession: D40984

R;Crossley, P.H.; Little, P.F.R.

Proc. Natl. Acad. Sci. U.S.A. 88, 7923-7927, 1991

A;Title: A cluster of related zinc finger protein genes is deleted in the mouse embryonic lethal mutation t(w18).

A;Reference number: A40984; MUID:91376058; PMID:1680234

A;Accession: D40984

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-39 <CRO>

A;Cross-references: GB:M74237

C;Keywords: DNA binding; zinc finger

Query Match	100.0%;	Score 30;	DB 2;	Length 39;
Best Local Similarity	100.0%;	Pred. No. 2.7;		

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQRVH 5  
|||||  
Db 23 HQRVH 27

RESULT 2

S10398

finger protein kox10 - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 21-Jul-2000

C;Accession: I37949; S10398

R;Thiesen, H.J.

New Biol. 2, 363-374, 1990

A;Title: Multiple genes encoding zinc finger domains are expressed in human T cells.

A;Reference number: I37949; MUID:91145339; PMID:2288909

A;Accession: I37949

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-56 <RES>

A;Cross-references: EMBL:X52341; NID:g34142; PIDN:CAA36567.1; PID:g930072

C;Genetics:

A;Gene: GDB:ZNF17; HPF3

A;Cross-references: GDB:125324

A;Map position: 19q-19q

C;Keywords: DNA binding; zinc finger

Query Match 100.0%; Score 30; DB 2; Length 56;

Best Local Similarity 100.0%; Pred. No. 3.9;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQRVH 5  
|||||  
Db 19 HQRVH 23

RESULT 3

I37960

zinc finger protein kox20 - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 12-Aug-1996 #sequence\_revision 12-Aug-1996 #text\_change 05-Nov-1999

C;Accession: I37960; S10409

R;Thiesen, H.J.

New Biol. 2, 363-374, 1990

A;Title: Multiple genes encoding zinc finger domains are expressed in human T cells.

A;Reference number: I37949; MUID:91145339; PMID:2288909

A;Accession: I37960

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-56 <RES>

A;Cross-references: EMBL:X52351; NID:g34153; PIDN:CAA36577.1; PID:g930083

C;Genetics:

A;Gene: GDB:ZNF26; KOX20

A;Cross-references: GDB:125333; OMIM:194537

A;Map position: 12q24.33-12q24.33  
C;Keywords: DNA binding; zinc finger

Query Match 100.0%; Score 30; DB 2; Length 56;  
Best Local Similarity 100.0%; Pred. No. 3.9;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQRVH 5  
|||||  
Db 47 HQRVH 51

RESULT 4

I37963

zinc finger protein kox23 - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 12-Aug-1996 #sequence\_revision 12-Aug-1996 #text\_change 05-Nov-1999

C;Accession: I37963; S10412

R;Thiesen, H.J.

New Biol. 2, 363-374, 1990

A;Title: Multiple genes encoding zinc finger domains are expressed in human T cells.

A;Reference number: I37949; MUID:91145339; PMID:2288909

A;Accession: I37963

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-56 <RES>

A;Cross-references: EMBL:X52354; NID:g34156; PIDN:CAA36580.1; PID:g930086

C;Keywords: DNA binding; zinc finger

F;3-51/Region: zinc finger

Query Match 100.0%; Score 30; DB 2; Length 56;  
Best Local Similarity 100.0%; Pred. No. 3.9;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQRVH 5  
|||||  
Db 47 HQRVH 51

RESULT 5

I37966

zinc finger protein kox26 - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 12-Aug-1996 #sequence\_revision 12-Aug-1996 #text\_change 05-Nov-1999

C;Accession: I37966; S10415

R;Thiesen, H.J.

New Biol. 2, 363-374, 1990

A;Title: Multiple genes encoding zinc finger domains are expressed in human T cells.

A;Reference number: I37949; MUID:91145339; PMID:2288909

A;Accession: I37966

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-56 <RES>

A;Cross-references: EMBL:X52357; NID:g34159; PIDN:CAA36583.1; PID:g930089

C;Genetics:

A;Gene: GDB:ZNF29  
A;Cross-references: GDB:125336; OMIM:194535  
A;Map position: 17pter-17p12  
C;Keywords: DNA binding; zinc finger

Query Match 100.0%; Score 30; DB 2; Length 56;  
Best Local Similarity 100.0%; Pred. No. 3.9;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQRVH 5  
|||||  
Db 47 HQRVH 51

RESULT 6

S47065

finger protein HZF7, Krueppel-related - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 21-Jul-2000

C;Accession: S47065; I37573

R;Abrink, M.; Aveskogh, M.; Hellman, L.

submitted to the EMBL Data Library, June 1994

A;Description: Isolation of cDNA clones for 42 different Krueppel-related zinc finger proteins encoded by the human genome.

A;Reference number: S47065

A;Accession: S47065

A;Molecule type: mRNA

A;Residues: 1-66 <ABR>

R;Abrink, M.; Aveskogh, M.; Hellman, L.

DNA Cell Biol. 14, 125-136, 1995

A;Title: Isolation of cDNA clones for 42 different Krueppel-related zinc finger proteins expressed in the human monoblast cell line U-937.

A;Reference number: I37566; MUID:95169271; PMID:7865130

A;Accession: I37573

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-66 <RES>

A;Cross-references: EMBL:X78930; NID:g498732; PIDN:CAA55530.1; PID:g836629

C;Genetics:

A;Gene: HZF7

C;Keywords: DNA binding; zinc finger

Query Match 100.0%; Score 30; DB 2; Length 66;  
Best Local Similarity 100.0%; Pred. No. 4.7;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQRVH 5  
|||||  
Db 7 HQRVH 11

RESULT 7

A42825

Kruppel-type zinc finger protein ZNF72 - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 01-Dec-2000

C;Accession: A42825



R;Aubry, M.; Marineau, C.; Zhang, F.R.; Zahed, L.; Figlewicz, D.; Delattre, O.; Thomas, G.; de Jong, P.J.; Julien, J.P.; Rouleau, G.A.  
Genomics 13, 641-648, 1992

A;Title: Cloning of six new genes with zinc finger motifs mapping to short and long arms of human acrocentric chromosome 22 (p and q11.2).

A;Reference number: A42825; MUID:92347859; PMID:1639391

A;Accession: A42825

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: nucleic acid

A;Residues: 1-85 <AUB>

A;Note: sequence extracted from NCBI backbone (NCBIP:109770)

C;Superfamily: zinc finger protein ZFP-36; LIM metal-binding repeat homology

Query Match 100.0%; Score 30; DB 2; Length 85;  
Best Local Similarity 100.0%; Pred. No. 6.1;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQRVH 5  
|||||  
Db 26 HQRVH 30

#### RESULT 8

I38941

zinc finger protein ZNF154 - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 23-Feb-1996 #sequence\_revision 23-Feb-1996 #text\_change 05-Nov-1999

C;Accession: I38941

R;Tommerup, N.; Vissing, H.

Genomics 27, 259-264, 1995

A;Title: Isolation and fine mapping of 16 novel human zinc finger-encoding cDNAs identify putative candidate genes for developmental and malignant disorders.

A;Reference number: A57785; MUID:96044430; PMID:7557990

A;Accession: I38941

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-87 <RES>

A;Cross-references: EMBL:U20648; NID:g676874; PIDN:AAC50257.1; PID:g676875

C;Genetics:

A;Gene: GDB:ZNF154

A;Cross-references: GDB:304989

A;Map position: 19q13.4-19q13.3

Query Match 100.0%; Score 30; DB 2; Length 87;  
Best Local Similarity 100.0%; Pred. No. 6.3;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQRVH 5  
|||||  
Db 25 HQRVH 29

#### RESULT 9

D43284

finger protein ZNF50 - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 20-Mar-1998

C;Accession: D43284  
 R;Lichter, P.; Bray, P.; Ried, T.; Dawid, I.B.; Ward, D.C.  
 Genomics 13, 999-1007, 1992  
 A;Title: Clustering of C2-H2 zinc finger motif sequences within telomeric and fragile site regions of human chromosomes.  
 A;Reference number: A43284; MUID:92372070; PMID:1505991  
 A;Accession: D43284  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-88 <LIC>  
 A;Cross-references: GB:M88360; NID:g340457; PID:g340458  
 A;Note: sequence extracted from NCBI backbone (NCBIN:111638, NCBIP:111639)  
 C;Keywords: zinc finger

Query Match 100.0%; Score 30; DB 2; Length 88;  
 Best Local Similarity 100.0%; Pred. No. 6.3;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQRVH 5  
 |||||  
 Db 1 HQRVH 5

# RESULT 10

B48827  
 zinc finger protein (clone CTfin92) - mouse (fragment)  
 C;Species: Mus musculus (house mouse)  
 C;Date: 01-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 05-Nov-1999  
 C;Accession: B48827  
 R;Noce, T.; Fujiwara, Y.; Sezaki, M.; Fujimoto, H.; Higashinakagawa, T.  
 Dev. Biol. 153, 356-367, 1992  
 A;Title: Expression of a mouse zinc finger protein gene in both spermatocytes and oocytes during meiosis.  
 A;Reference number: A48827; MUID:93012481; PMID:1397691  
 A;Accession: B48827  
 A;Status: preliminary; not compared with conceptual translation  
 A;Molecule type: mRNA  
 A;Residues: 1-105 <NOC>  
 A;Cross-references: GB:D10631; NID:g220644; PIDN:BAA01481.1; PID:d1001956; PID:g220645  
 A;Experimental source: spermatogenic cells  
 A;Note: sequence extracted from NCBI backbone (NCBIP:114772)  
 C;Keywords: DNA binding; transcription regulation

Query Match 100.0%; Score 30; DB 2; Length 105;  
 Best Local Similarity 100.0%; Pred. No. 7.6;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQRVH 5  
 |||||  
 Db 17 HQRVH 21

# RESULT 11

D31201  
 GLI-related finger protein HKR2 - human (fragment)  
 C;Species: Homo sapiens (man)

C;Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 02-Aug-1996  
C;Accession: D31201  
R;Ruppert, J.M.; Kinzler, K.W.; Wong, A.J.; Bigner, S.H.; Kao, F.T.; Law, M.L.;  
Seuanez, H.N.; O'Brien, S.J.; Vogelstein, B.  
Mol. Cell. Biol. 8, 3104-3113, 1988  
A;Title: The GLI-Kruppel family of human genes.  
A;Reference number: A93103; MUID:89096896; PMID:2850480  
A;Accession: D31201  
A;Molecule type: DNA  
A;Residues: 1-106 <RUP>  
C;Keywords: DNA binding; tandem repeat; zinc finger

Query Match 100.0%; Score 30; DB 2; Length 106;  
Best Local Similarity 100.0%; Pred. No. 7.7;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQRVH 5  
|||||  
Db 77 HQRVH 81

RESULT 12

T34560

hypothetical protein DKFZp434J0650.1 - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 29-Oct-1999

C;Accession: T34560

R;Poustka, A.; Wellenreuther, R.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.  
submitted to the Protein Sequence Database, October 1999

A;Reference number: Z21540

A;Accession: T34560

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-106 <POU>

A;Cross-references: EMBL:AL122078

A;Experimental source: adult testis; clone DKFZp434J0650

C;Genetics:

A;Note: DKFZp434J0650.1

Query Match 100.0%; Score 30; DB 2; Length 106;  
Best Local Similarity 100.0%; Pred. No. 7.7;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQRVH 5  
|||||  
Db 44 HQRVH 48

RESULT 13

QQBED9

HHLF3 protein - human cytomegalovirus (strain AD169)

N;Alternate names: hypothetical protein US33

C;Species: human cytomegalovirus, human herpesvirus 5

C;Date: 30-Sep-1989 #sequence\_revision 30-Sep-1989 #text\_change 28-Jul-2000

C;Accession: I27216; S09948

R;Weston, K.; Barrell, B.G.

J. Mol. Biol. 192, 177-208, 1986

A;Title: Sequence of the short unique region, short repeats, and part of the long repeats of human cytomegalovirus.  
 A;Reference number: A92935; MUID:87169717; PMID:3031311  
 A;Accession: I27216  
 A;Molecule type: DNA  
 A;Residues: 1-137 <WES>  
 A;Cross-references: EMBL:X04650; NID:g59801; PIDN:CAB37119.1; PID:g4456201  
 A;Experimental source: strain AD169  
 R;Chee, M.S.; Bankier, A.T.; Beck, S.; Bohni, R.; Brown, C.M.; Cerny, R.; Horsnell, T.; Hutchison III, C.A.; Kouzarides, T.; Martignetti, J.A.; Preddie, E.; Satchwell, S.C.; Tomlinson, P.; Weston, K.M.; Barrell, B.G.  
 Curr. Top. Microbiol. Immunol. 154, 125-169, 1990  
 A;Title: Analysis of the protein-coding content of the sequence of human cytomegalovirus strain AD169.  
 A;Reference number: S09749; MUID:90269039; PMID:2161319  
 A;Accession: S09948  
 A;Status: nucleic acid sequence not shown; translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-137 <CHE>  
 A;Cross-references: EMBL:X17403; NID:g59591; PIDN:CAA35266.1; PID:g1780965  
 A;Experimental source: strain AD169  
 A;Note: this sequence was submitted to the EMBL Data Library, December 1989  
 A;Note: this reading frame extends between two stop codons and does not begin with a start codon  
 C;Genetics:  
 A;Gene: HHLF3  
 C;Superfamily: cytomegalovirus HHLF3 protein

Query Match 100.0%; Score 30; DB 1; Length 137;  
 Best Local Similarity 100.0%; Pred. No. 10;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQRVH 5  
 |||||  
 Db 72 HQRVH 76

#### RESULT 14

I38620

zinc finger protein ZNF155 - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 23-Feb-1996 #sequence\_revision 23-Feb-1996 #text\_change 05-Nov-1999

C;Accession: I38620

R;Tommerup, N.; Vissing, H.

Genomics 27, 259-264, 1995

A;Title: Isolation and fine mapping of 16 novel human zinc finger-encoding cDNAs identify putative candidate genes for developmental and malignant disorders.

A;Reference number: A57785; MUID:96044430; PMID:7557990

A;Accession: I38620

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-139 <RES>

A;Cross-references: EMBL:U09852; NID:g495575; PIDN:AAC50268.1; PID:g495576

C;Genetics:

A;Gene: GDB:ZNF155

A;Cross-references: GDB:304990

A;Map position: 19q13.2-19q13.32

Query Match 100.0%; Score 30; DB 2; Length 139;  
Best Local Similarity 100.0%; Pred. No. 10;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQRVH 5  
|||||  
Db 65 HQRVH 69

RESULT 15

A39240

finger protein mfg1 - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 04-Oct-1991 #sequence\_revision 04-Oct-1991 #text\_change 05-Nov-1999

C;Accession: A39240

R;Passananti, C.; Felsani, A.; Caruso, M.; Amati, P.

Proc. Natl. Acad. Sci. U.S.A. 86, 9417-9421, 1989

A;Title: Mouse genes coding for "zinc-finger"-containing proteins:  
characterization and expression in differentiated cells.

A;Reference number: A39240; MUID:90083278; PMID:2512579

A;Accession: A39240

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-169 <PAS>

A;Cross-references: GB:M28513; NID:g199136; PIDN:AAA39531.1; PID:g554203

C;Keywords: DNA binding; zinc finger

Query Match 100.0%; Score 30; DB 2; Length 169;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQRVH 5  
|||||  
Db 54 HQRVH 58

Search completed: March 5, 2004, 16:28:55

Job time : 2.14198 secs

OM protein - protein search, using sw model

Run on: March 5, 2004, 16:22:54 ; Search time 2.70062 Seconds  
(without alignments)  
390.935 Million cell updates/sec

Title: US-10-057-890A-7  
Perfect score: 30  
Sequence: 1 HQRVH 5

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 809742 seqs, 211153259 residues

Total number of hits satisfying chosen parameters: 809742

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*
- 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep:\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep:\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep:\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep:\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result		Query				Description
No.	Score	Match Length	DB	ID		

1	30	100.0	5	14	US-10-057-890A-7	Sequence 7, Appli
2	30	100.0	23	14	US-10-223-765-181	Sequence 181, App
3	30	100.0	23	14	US-10-314-669-103	Sequence 103, App
4	30	100.0	23	15	US-10-074-978A-123	Sequence 123, App
5	30	100.0	23	15	US-10-074-978A-124	Sequence 124, App
6	30	100.0	23	15	US-10-074-978A-125	Sequence 125, App
7	30	100.0	23	15	US-10-074-978A-126	Sequence 126, App
8	30	100.0	23	15	US-10-074-978A-127	Sequence 127, App
9	30	100.0	30	9	US-09-864-761-43845	Sequence 43845, A
10	30	100.0	51	14	US-10-029-386-29892	Sequence 29892, A
11	30	100.0	52	14	US-10-029-386-29011	Sequence 29011, A
12	30	100.0	79	14	US-10-029-386-33598	Sequence 33598, A
13	30	100.0	88	9	US-09-764-864-1488	Sequence 1488, Ap
14	30	100.0	93	11	US-09-833-245-304	Sequence 304, App
15	30	100.0	93	14	US-10-144-156-2	Sequence 2, Appli
16	30	100.0	99	14	US-10-029-386-30335	Sequence 30335, A
17	30	100.0	114	9	US-09-764-864-1372	Sequence 1372, Ap
18	30	100.0	115	9	US-09-925-300-1555	Sequence 1555, Ap
19	30	100.0	120	9	US-09-764-864-970	Sequence 970, App
20	30	100.0	125	9	US-09-764-853-815	Sequence 815, App
21	30	100.0	126	9	US-09-864-761-43918	Sequence 43918, A
22	30	100.0	127	10	US-09-820-649-238	Sequence 238, App
23	30	100.0	127	14	US-10-160-162-238	Sequence 238, App
24	30	100.0	135	14	US-10-106-698-6455	Sequence 6455, Ap
25	30	100.0	138	14	US-10-057-890A-10	Sequence 10, Appl
26	30	100.0	144	15	US-10-108-260A-2472	Sequence 2472, Ap
27	30	100.0	145	15	US-10-104-047-2556	Sequence 2556, Ap
28	30	100.0	153	15	US-10-104-047-3007	Sequence 3007, Ap
29	30	100.0	154	9	US-09-764-864-1321	Sequence 1321, Ap
30	30	100.0	157	14	US-10-057-890A-31	Sequence 31, Appl
31	30	100.0	165	9	US-09-764-864-1486	Sequence 1486, Ap
32	30	100.0	166	9	US-09-764-864-1472	Sequence 1472, Ap
33	30	100.0	167	15	US-10-108-260A-3344	Sequence 3344, Ap
34	30	100.0	180	9	US-09-864-761-36704	Sequence 36704, A
35	30	100.0	183	15	US-10-074-978A-115	Sequence 115, App
36	30	100.0	184	15	US-10-104-047-2477	Sequence 2477, Ap
37	30	100.0	184	15	US-10-108-260A-3787	Sequence 3787, Ap
38	30	100.0	184	15	US-10-108-260A-4369	Sequence 4369, Ap
39	30	100.0	184	15	US-10-074-978A-114	Sequence 114, App
40	30	100.0	190	15	US-10-264-049-2671	Sequence 2671, Ap
41	30	100.0	191	9	US-09-764-864-1358	Sequence 1358, Ap
42	30	100.0	192	9	US-09-764-864-1046	Sequence 1046, Ap
43	30	100.0	192	9	US-09-764-864-1473	Sequence 1473, Ap
44	30	100.0	198	15	US-10-108-260A-3472	Sequence 3472, Ap
45	30	100.0	211	14	US-10-029-386-34052	Sequence 34052, A

#### ALIGNMENTS

RESULT 1  
 US-10-057-890A-7  
 ; Sequence 7, Application US/10057890A  
 ; Publication No. US20030044901A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Coleman, Timothy

```
; APPLICANT: Mansfield, Brian
; TITLE OF INVENTION: Scaffold Fusion Polypeptides, Composition for Making the
Same, and Methods
; TITLE OF INVENTION: of Using the Same.
; FILE REFERENCE: PF537
; CURRENT APPLICATION NUMBER: US/10/057,890A
; CURRENT FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: 60/265,782
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,858
; PRIOR FILING DATE: 2001-01-31
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 7
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-057-890A-7
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Query Match          100.0%; Score 30; DB 14; Length 5;
Best Local Similarity 100.0%; Pred. No. 7.1e+05;
Matches      5; Conservative    0; Mismatches    0; Indels      0; Gaps      0;
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```
Qy      1 HQRVH 5
        |||||
Db      1 HQRVH 5
```

#### RESULT 2

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US-10-223-765-181
; Sequence 181, Application US/10223765
; Publication No. US20030165997A1
; GENERAL INFORMATION:
; APPLICANT: Kim, Jin-Soo
; APPLICANT: Bae, Kwang-Hee
; APPLICANT: Park, Kyung-Soon
; APPLICANT: Kwon, Young Do
; APPLICANT: Ryu, Eun-Hyun
; APPLICANT: Hwang, Moon-Sun
; TITLE OF INVENTION: ZINC FINGER DOMAIN LIBRARIES
; FILE REFERENCE: 12279-005001
; CURRENT APPLICATION NUMBER: US/10/223,765
; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: 60/374,355
; PRIOR FILING DATE: 2002-04-22
; PRIOR APPLICATION NUMBER: 60/313,402
; PRIOR FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 181
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-223-765-181
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```
Query Match          100.0%; Score 30; DB 14; Length 23;
Best Local Similarity 100.0%; Pred. No. 22;
Matches      5; Conservative    0; Mismatches    0; Indels      0; Gaps      0;
```



Qy 1 HQRVH 5  
|||||  
Db 19 HQRVH 23

RESULT 3

US-10-314-669-103  
; Sequence 103, Application US/10314669  
; Publication No. US20030194727A1  
; GENERAL INFORMATION:  
; APPLICANT: Kim, Jin-Soo  
; APPLICANT: Park, Kyung-Soon  
; APPLICANT: Lee, Dong-Ki  
; APPLICANT: Seol, Wongi  
; APPLICANT: Lee, Horim  
; APPLICANT: Lee, Seong-il  
; APPLICANT: Yang, Hyo-Young  
; APPLICANT: Lee, Yangsoon  
; APPLICANT: Jang, Young-Soon  
; TITLE OF INVENTION: PHENOTYPIC SCREEN OF CHIMERIC PROTEINS  
; FILE REFERENCE: 12279-007001  
; CURRENT APPLICATION NUMBER: US/10/314,669  
; CURRENT FILING DATE: 2002-12-09  
; PRIOR APPLICATION NUMBER: US 60/338,441  
; PRIOR FILING DATE: 2001-12-07  
; PRIOR APPLICATION NUMBER: US 60/376,053  
; PRIOR FILING DATE: 2002-04-26  
; PRIOR APPLICATION NUMBER: US 60/400,904  
; PRIOR FILING DATE: 2002-08-02  
; PRIOR APPLICATION NUMBER: US 60/401,089  
; PRIOR FILING DATE: 2002-08-05  
; NUMBER OF SEQ ID NOS: 266  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 103  
; LENGTH: 23  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-314-669-103

Query Match 100.0%; Score 30; DB 14; Length 23;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQRVH 5  
|||||  
Db 19 HQRVH 23

RESULT 4

US-10-074-978A-123  
; Sequence 123, Application US/10074978A  
; Publication No. US20040010119A1  
; GENERAL INFORMATION:  
; APPLICANT: Leite, Mario  
; APPLICANT: Spytek, Kimberly A  
; APPLICANT: Guo, Xiaojia (Sasha)

; APPLICANT: Fernandes, Elma  
; APPLICANT: Li, Li  
; APPLICANT: Kekuda, Ramesh  
; APPLICANT: Liu, Xiahong  
; APPLICANT: Casman, Stacie  
; APPLICANT: Boldog, Ferenc  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Blalock, Angela  
; APPLICANT: Ballinger, Robert  
; APPLICANT: Vernet, Corine  
; APPLICANT: Tchernev, Velizar T  
; APPLICANT: Malyankar, Uriel M  
; APPLICANT: Gusev, Vladimir  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Mezes, Peter S  
; APPLICANT: Ellerman, Karen  
; APPLICANT: Heyes, Melvin P  
; APPLICANT: Herrman, John  
; APPLICANT: Pena, Carol E A  
; APPLICANT: Shimkets, Richard A  
; APPLICANT: Taupier Jr, Raymond J  
; APPLICANT: Moore, No. US20040010119A111e  
; APPLICANT: Shenoy, Suresh  
; APPLICANT: Edinger, Shlomit  
; APPLICANT: Gunther, Erik  
; APPLICANT: Stone, Dave  
; APPLICANT: Millet, Isabelle  
; APPLICANT: Peyman, John  
; APPLICANT: Smithson, Glennda  
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME  
; FILE REFERENCE: 21402-269  
; CURRENT APPLICATION NUMBER: US/10/074,978A  
; CURRENT FILING DATE: 2003-01-07  
; PRIOR APPLICATION NUMBER: 60/268,221  
; PRIOR FILING DATE: 2001-02-12  
; PRIOR APPLICATION NUMBER: 60/335,109  
; PRIOR FILING DATE: 2001-10-31  
; PRIOR APPLICATION NUMBER: 60/312,284  
; PRIOR FILING DATE: 2001-08-14  
; PRIOR APPLICATION NUMBER: 60/268,496  
; PRIOR FILING DATE: 2001-02-13  
; PRIOR APPLICATION NUMBER: 60/276,703  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/330,293  
; PRIOR FILING DATE: 2001-10-18  
; PRIOR APPLICATION NUMBER: 60/322,127  
; PRIOR FILING DATE: 2001-11-21  
; PRIOR APPLICATION NUMBER: 60/280,899  
; PRIOR FILING DATE: 2001-04-02  
; PRIOR APPLICATION NUMBER: 60/310,797  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: 60/268,646  
; PRIOR FILING DATE: 2001-02-14  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 547  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 123

; LENGTH: 23  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-074-978A-123

Query Match 100.0%; Score 30; DB 15; Length 23;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HQRVH 5  
|||||  
Db 19 HQRVH 23

RESULT 5

US-10-074-978A-124

; Sequence 124, Application US/10074978A

; Publication No. US20040010119A1

; GENERAL INFORMATION:

; APPLICANT: Leite, Mario  
; APPLICANT: Spytek, Kimberly A  
; APPLICANT: Guo, Xiaojia (Sasha)  
; APPLICANT: Fernandes, Elma  
; APPLICANT: Li, Li  
; APPLICANT: Kekuda, Ramesh  
; APPLICANT: Liu, Xiahong  
; APPLICANT: Casman, Stacie  
; APPLICANT: Boldog, Ferenc  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Blalock, Angela  
; APPLICANT: Ballinger, Robert  
; APPLICANT: Vernet, Corine  
; APPLICANT: Tchernev, Velizar T  
; APPLICANT: Malyankar, Uriel M  
; APPLICANT: Gusev, Vladimir  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Mezes, Peter S  
; APPLICANT: Ellerman, Karen  
; APPLICANT: Heyes, Melvin P  
; APPLICANT: Herrman, John  
; APPLICANT: Pena, Carol E A  
; APPLICANT: Shimkets, Richard A  
; APPLICANT: Taupier Jr, Raymond J  
; APPLICANT: Moore, No. US20040010119A1lle  
; APPLICANT: Shenoy, Suresh  
; APPLICANT: Edinger, Shlomit  
; APPLICANT: Gunther, Erik  
; APPLICANT: Stone, Dave  
; APPLICANT: Millet, Isabelle  
; APPLICANT: Peyman, John  
; APPLICANT: Smithson, Glennda

; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME

; FILE REFERENCE: 21402-269

; CURRENT APPLICATION NUMBER: US/10/074,978A

; CURRENT FILING DATE: 2003-01-07

; PRIOR APPLICATION NUMBER: 60/268,221

; PRIOR FILING DATE: 2001-02-12

```

; PRIOR APPLICATION NUMBER: 60/335,109
; PRIOR FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: 60/312,284
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: 60/268,496
; PRIOR FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 60/276,703
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/330,293
; PRIOR FILING DATE: 2001-10-18
; PRIOR APPLICATION NUMBER: 60/322,127
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/280,899
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 60/310,797
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/268,646
; PRIOR FILING DATE: 2001-02-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 124
;   LENGTH: 23
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-074-978A-124

```

```

Query Match          100.0%; Score 30; DB 15; Length 23;
Best Local Similarity 100.0%; Pred. No. 22;
Matches      5; Conservative    0; Mismatches    0; Indels      0; Gaps      0;

```

```

Qy          1 HQRVH 5
             |||||
Db          19 HQRVH 23

```

# RESULT 6

```

US-10-074-978A-125
; Sequence 125, Application US/10074978A
; Publication No. US20040010119A1
; GENERAL INFORMATION:
; APPLICANT: Leite, Mario
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Fernandes, Elma
; APPLICANT: Li, Li
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Liu, Xiahong
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ferenc
; APPLICANT: Patturajan, Meera
; APPLICANT: Blalock, Angela
; APPLICANT: Ballinger, Robert
; APPLICANT: Vernet, Corine
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Gusev, Vladimir

```

```

; APPLICANT: Rastelli, Luca
; APPLICANT: Mezes, Peter S
; APPLICANT: Ellerman, Karen
; APPLICANT: Heyes, Melvin P
; APPLICANT: Herrman, John
; APPLICANT: Pena, Carol E A
; APPLICANT: Shimkets, Richard A
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Moore, No. US20040010119A1lle
; APPLICANT: Shenoy, Suresh
; APPLICANT: Edinger, Shlomit
; APPLICANT: Gunther, Erik
; APPLICANT: Stone, Dave
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John
; APPLICANT: Smithson, Glennnda
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-269
; CURRENT APPLICATION NUMBER: US/10/074,978A
; CURRENT FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: 60/268,221
; PRIOR FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/335,109
; PRIOR FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: 60/312,284
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: 60/268,496
; PRIOR FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 60/276,703
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/330,293
; PRIOR FILING DATE: 2001-10-18
; PRIOR APPLICATION NUMBER: 60/322,127
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/280,899
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 60/310,797
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/268,646
; PRIOR FILING DATE: 2001-02-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 125
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-074-978A-125

```

```

Query Match          100.0%; Score 30; DB 15; Length 23;
Best Local Similarity 100.0%; Pred. No. 22;
Matches      5; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      1 HQRVH 5
        |||||
Db      19 HQRVH 23

```

RESULT 7

US-10-074-978A-126

; Sequence 126, Application US/10074978A

; Publication No. US20040010119A1

; GENERAL INFORMATION:

; APPLICANT: Leite, Mario

; APPLICANT: Spytek, Kimberly A

; APPLICANT: Guo, Xiaojia (Sasha)

; APPLICANT: Fernandes, Elma

; APPLICANT: Li, Li

; APPLICANT: Kekuda, Ramesh

; APPLICANT: Liu, Xiahong

; APPLICANT: Casman, Stacie

; APPLICANT: Boldog, Ferenc

; APPLICANT: Patturajan, Meera

; APPLICANT: Blalock, Angela

; APPLICANT: Ballinger, Robert

; APPLICANT: Vernet, Corine

; APPLICANT: Tchernev, Velizar T

; APPLICANT: Malyankar, Uriel M

; APPLICANT: Gusev, Vladimir

; APPLICANT: Rastelli, Luca

; APPLICANT: Mezes, Peter S

; APPLICANT: Ellerman, Karen

; APPLICANT: Heyes, Melvin P

; APPLICANT: Herrman, John

; APPLICANT: Pena, Carol E A

; APPLICANT: Shimkets, Richard A

; APPLICANT: Taupier Jr, Raymond J

; APPLICANT: Moore, No. US20040010119A111e

; APPLICANT: Shenoy, Suresh

; APPLICANT: Edinger, Shlomit

; APPLICANT: Gunther, Erik

; APPLICANT: Stone, Dave

; APPLICANT: Millet, Isabelle

; APPLICANT: Peyman, John

; APPLICANT: Smithson, Glennnda

; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME

; FILE REFERENCE: 21402-269

; CURRENT APPLICATION NUMBER: US/10/074,978A

; CURRENT FILING DATE: 2003-01-07

; PRIOR APPLICATION NUMBER: 60/268,221

; PRIOR FILING DATE: 2001-02-12

; PRIOR APPLICATION NUMBER: 60/335,109

; PRIOR FILING DATE: 2001-10-31

; PRIOR APPLICATION NUMBER: 60/312,284

; PRIOR FILING DATE: 2001-08-14

; PRIOR APPLICATION NUMBER: 60/268,496

; PRIOR FILING DATE: 2001-02-13

; PRIOR APPLICATION NUMBER: 60/276,703

; PRIOR FILING DATE: 2001-03-16

; PRIOR APPLICATION NUMBER: 60/330,293

; PRIOR FILING DATE: 2001-10-18

; PRIOR APPLICATION NUMBER: 60/322,127

; PRIOR FILING DATE: 2001-11-21

; PRIOR APPLICATION NUMBER: 60/280,899

```
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 60/310,797
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/268,646
; PRIOR FILING DATE: 2001-02-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 126
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-074-978A-126
```

```
Query Match          100.0%; Score 30; DB 15; Length 23;
Best Local Similarity 100.0%; Pred. No. 22;
Matches      5; Conservative    0; Mismatches    0; Indels    0; Gaps    0;
```

```
Qy      1 HQRVH 5
        |||||
Db      19 HQRVH 23
```

# RESULT 8

```
US-10-074-978A-127
; Sequence 127, Application US/10074978A
; Publication No. US20040010119A1
; GENERAL INFORMATION:
; APPLICANT: Leite, Mario
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Fernandes, Elma
; APPLICANT: Li, Li
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Liu, Xiahong
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ferenc
; APPLICANT: Patturajan, Meera
; APPLICANT: Blalock, Angela
; APPLICANT: Ballinger, Robert
; APPLICANT: Vernet, Corine
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Gusev, Vladimir
; APPLICANT: Rastelli, Luca
; APPLICANT: Mezes, Peter S
; APPLICANT: Ellerman, Karen
; APPLICANT: Heyes, Melvin P
; APPLICANT: Herrman, John
; APPLICANT: Pena, Carol E A
; APPLICANT: Shimkets, Richard A
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Moore, No. US20040010119A111e
; APPLICANT: Shenoy, Suresh
; APPLICANT: Edinger, Shlomit
; APPLICANT: Gunther, Erik
; APPLICANT: Stone, Dave
```

```

; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John
; APPLICANT: Smithson, Glennnda
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-269
; CURRENT APPLICATION NUMBER: US/10/074,978A
; CURRENT FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: 60/268,221
; PRIOR FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/335,109
; PRIOR FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: 60/312,284
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: 60/268,496
; PRIOR FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 60/276,703
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/330,293
; PRIOR FILING DATE: 2001-10-18
; PRIOR APPLICATION NUMBER: 60/322,127
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/280,899
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 60/310,797
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/268,646
; PRIOR FILING DATE: 2001-02-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 127
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-074-978A-127

```

```

Query Match          100.0%; Score 30; DB 15; Length 23;
Best Local Similarity 100.0%; Pred. No. 22;
Matches      5; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      1 HQRVH 5
        |||||
Db      19 HQRVH 23

```

RESULT 9

```

US-09-864-761-43845
; Sequence 43845, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES
USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

```



```

; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 43845
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC005324.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.62
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.6
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.84
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.78
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.86
; OTHER INFORMATION: SWISSPROT HIT: O60765, EVALUE 3.00e-08
; OTHER INFORMATION: EST_HUMAN HIT: BE902618.1, EVALUE 6.00e-12
US-09-864-761-43845

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Query Match 100.0%; Score 30; DB 9; Length 30;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQRVH 5  
|||||  
Db 21 HQRVH 25

RESULT 10

US-10-029-386-29892  
; Sequence 29892, Application US/10029386  
; Publication No. US20030194704A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharron G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES  
USEFUL FOR GENE  
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO  
; FILE REFERENCE: AEOMICA-X-2  
; CURRENT APPLICATION NUMBER: US/10/029,386  
; CURRENT FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 34288  
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 29892  
; LENGTH: 51  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO CHR1.1  
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.9  
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.97  
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.81  
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.1  
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.76  
; OTHER INFORMATION: SWISSPROT HIT: Q9NYT6, EVALUATE 1.00e-26  
US-10-029-386-29892

Query Match 100.0%; Score 30; DB 14; Length 51;  
Best Local Similarity 100.0%; Pred. No. 45;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQRVH 5  
|||||  
Db 6 HQRVH 10

RESULT 11

US-10-029-386-29011  
; Sequence 29011, Application US/10029386  
; Publication No. US20030194704A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharron G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.

```

; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES
USEFUL FOR GENE
; TITLE OF INVENTION:  EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE:  2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 29011
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR1.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.78
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.54
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.5
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.44
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.96
; OTHER INFORMATION: SWISSPROT HIT: Q9UL59, EVALUE 7.00e-20
US-10-029-386-29011

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```

Query Match          100.0%;  Score 30;  DB 14;  Length 52;
Best Local Similarity 100.0%;  Pred. No. 46;
Matches      5;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

```

Qy      1 HQRVH 5
        |||||
Db      17 HQRVH 21

```

# RESULT 12

US-10-029-386-33598

```

; Sequence 33598, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES
USEFUL FOR GENE
; TITLE OF INVENTION:  EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE:  2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 33598
; LENGTH: 79
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR1.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.7
; OTHER INFORMATION: SWISSPROT HIT: Q61116, EVALUE 1.00e-41

```

US-10-029-386-33598

Query Match 100.0%; Score 30; DB 14; Length 79;  
Best Local Similarity 100.0%; Pred. No. 68;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQRVH 5  
|||||  
Db 56 HQRVH 60

RESULT 13

US-09-764-864-1488  
; Sequence 1488, Application US/09764864  
; Patent No. US20020132753A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PTZ23  
; CURRENT APPLICATION NUMBER: US/09/764,864  
; CURRENT FILING DATE: 2001-01-17  
; Prior application data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 1792  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1488  
; LENGTH: 88  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-764-864-1488

Query Match 100.0%; Score 30; DB 9; Length 88;  
Best Local Similarity 100.0%; Pred. No. 75;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQRVH 5  
|||||  
Db 54 HQRVH 58

RESULT 14

US-09-833-245-304  
; Sequence 304, Application US/09833245  
; Publication No. US20040010134A1  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; TITLE OF INVENTION: Albumin Fusion Proteins  
; FILE REFERENCE: PF546PCT  
; CURRENT APPLICATION NUMBER: US/09/833,245  
; CURRENT FILING DATE: 2001-04-12  
; PRIOR APPLICATION NUMBER: 60/229, 358  
; PRIOR FILING DATE: 2000-04-12  
; PRIOR APPLICATION NUMBER: 60/256, 931  
; PRIOR FILING DATE: 2000-12-21  
; PRIOR APPLICATION NUMBER: 60/199, 384  
; PRIOR FILING DATE: 2000-04-25  
; NUMBER OF SEQ ID NOS: 2267  
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 304  
; LENGTH: 93  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (5)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-09-833-245-304

Query Match 100.0%; Score 30; DB 11; Length 93;  
Best Local Similarity 100.0%; Pred. No. 79;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQRVH 5  
|||||  
Db 56 HQRVH 60

RESULT 15

US-10-144-156-2

; Sequence 2, Application US/10144156  
; Publication No. US20030166197A1  
; GENERAL INFORMATION:  
; APPLICANT: Ecker, Joseph R.  
; APPLICANT: Nehring, Ramlah  
; APPLICANT: McGrath, Robert B.  
; TITLE OF INVENTION: ETHYLENE INSENSITIVE PLANTS  
; FILE REFERENCE: SALKINS.040A  
; CURRENT APPLICATION NUMBER: US/10/144,156  
; CURRENT FILING DATE: 2002-05-10  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 93  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; NAME/KEY: ZN\_FING  
; LOCATION: (1)...(93)  
US-10-144-156-2

Query Match 100.0%; Score 30; DB 14; Length 93;  
Best Local Similarity 100.0%; Pred. No. 79;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQRVH 5  
|||||  
Db 23 HQRVH 27

Search completed: March 5, 2004, 16:33:42  
Job time : 2.70062 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 5, 2004, 16:15:44 ; Search time 3.3179 Seconds  
(without alignments)  
475.479 Million cell updates/sec

Title: US-10-057-890A-7  
Perfect score: 30  
Sequence: 1 HQRVH 5

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_25:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvirus:\*  
16: sp\_bacteriaphage:\*  
17: sp\_archaea:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query	Match	Length	DB	ID	Description
No.							

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1	30	100.0	48	11	P97663	P97663 rattus norv
2	30	100.0	53	4	O14850	O14850 homo sapien
3	30	100.0	57	11	O88233	O88233 mus musculu
4	30	100.0	57	11	Q9QWM7	Q9qwm7 mus musculu
5	30	100.0	57	11	Q9QWN0	Q9qwn0 mus musculu
6	30	100.0	70	4	O14886	O14886 homo sapien
7	30	100.0	74	4	O14887	O14887 homo sapien
8	30	100.0	74	4	O14888	O14888 homo sapien
9	30	100.0	75	4	O14890	O14890 homo sapien
10	30	100.0	85	11	O88258	O88258 mus musculu
11	30	100.0	85	11	O88253	O88253 mus musculu
12	30	100.0	88	4	Q15922	Q15922 homo sapien
13	30	100.0	92	11	Q8C2B8	Q8c2b8 mus musculu
14	30	100.0	102	4	O14899	O14899 homo sapien
15	30	100.0	106	4	Q9UFH1	Q9ufh1 homo sapien
16	30	100.0	107	11	Q60916	Q60916 mus musculu
17	30	100.0	130	6	Q95286	Q95286 sus scrofa
18	30	100.0	131	16	Q8DA53	Q8da53 vibrio vuln
19	30	100.0	137	6	Q29240	Q29240 sus scrofa
20	30	100.0	139	4	Q86WM3	Q86wm3 homo sapien
21	30	100.0	145	4	Q8NB43	Q8nb43 homo sapien
22	30	100.0	151	6	Q9XSR2	Q9xsr2 canis famil
23	30	100.0	153	4	Q8TCQ7	Q8tcq7 homo sapien
24	30	100.0	153	16	Q8PJP7	Q8pjp7 xanthomonas
25	30	100.0	153	16	Q8P892	Q8p892 xanthomonas
26	30	100.0	167	4	Q8N932	Q8n932 homo sapien
27	30	100.0	175	11	Q9ES79	Q9es79 mus musculu
28	30	100.0	179	11	Q9JJR2	Q9jjr2 mus musculu
29	30	100.0	184	4	Q15914	Q15914 homo sapien
30	30	100.0	198	4	Q8N8Y5	Q8n8y5 homo sapien
31	30	100.0	198	11	Q8BSV7	Q8bsv7 mus musculu
32	30	100.0	199	4	Q9NWL3	Q9nwl3 homo sapien
33	30	100.0	201	11	Q99J71	Q99j71 mus musculu
34	30	100.0	205	4	Q15918	Q15918 homo sapien
35	30	100.0	205	4	Q9H707	Q9h707 homo sapien
36	30	100.0	206	5	Q9VEK2	Q9vek2 drosophila
37	30	100.0	207	4	Q8NDL8	Q8ndl8 homo sapien
38	30	100.0	208	4	Q8N4Z8	Q8n4z8 homo sapien
39	30	100.0	225	4	Q86WM2	Q86wm2 homo sapien
40	30	100.0	229	4	Q8N506	Q8n506 homo sapien
41	30	100.0	230	4	Q9BTG0	Q9btg0 homo sapien
42	30	100.0	230	4	Q96IT2	Q96it2 homo sapien
43	30	100.0	232	16	Q87VP6	Q87vp6 pseudomonas
44	30	100.0	250	4	Q7Z331	Q7z331 homo sapien
45	30	100.0	251	16	Q8PJQ1	Q8pjql xanthomonas

# ALIGNMENTS

## RESULT 1

P97663

ID P97663 PRELIMINARY; PRT; 48 AA.

AC P97663;

DT 01-JAN-1998 (TrEMBLrel. 05, Created)

DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Zinc finger protein 7 (Fragment).  
 GN DZF7.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96319713; PubMed=8697448;  
 RA Gebelein B., Mesa K., Urrutia R.;  
 RT "A novel profile of expressed sequence tags for zinc finger encoding  
 RT genes from the poorly differentiated exocrine pancreatic cell line  
 RT AR4IP.";  
 RL Cancer Lett. 105:225-231(1996).  
 DR EMBL; U78135; AAB36807.1; -.  
 DR InterPro; IPR007087; Znf\_C2H2.  
 DR InterPro; IPR007086; Znf\_C2H2\_sub.  
 DR Pfam; PF00096; zf-C2H2; 1.  
 DR PRINTS; PR00048; ZINCFINGER.  
 DR ProDom; PD000003; Znf\_C2H2; 1.  
 DR SMART; SM00355; Znf\_C2H2; 1.  
 DR PROSITE; PS00028; ZINC\_FINGER\_C2H2\_1; 1.  
 DR PROSITE; PS50157; ZINC\_FINGER\_C2H2\_2; 2.  
 KW Metal-binding; Zinc; Zinc-finger.  
 FT NON\_TER 1 1  
 FT NON\_TER 48 48  
 SQ SEQUENCE 48 AA; 5388 MW; 3A5A7EA34459B06A CRC64;

Query Match 100.0%; Score 30; DB 11; Length 48;  
 Best Local Similarity 100.0%; Pred. No. 14;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HQRVH 5  
 |||||  
 Db 39 HQRVH 43

## RESULT 2

O14850

ID O14850 PRELIMINARY; PRT; 53 AA.  
 AC O14850;  
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Zinc finger protein (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RA Wu G., Yu L., Sun X., Wu M., Fan Y., Jiang C., Zheng Q., Zhang Q.,  
 RA Zhao S.;  
 RT "Isolation and Cloning of Novel C2-H2 Type Zinc Finger Protein Gene in  
 RT Human Liver Tissue.";  
 RL Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.



CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
 DR EMBL; AF024698; AAB81088.1; -.  
 DR GO; GO:0005634; C:nucleus; IEA.  
 DR InterPro; IPR007087; Znf\_C2H2.  
 DR InterPro; IPR007086; Znf\_C2H2\_sub.  
 DR Pfam; PF00096; zf-C2H2; 1.  
 DR PRINTS; PR00048; ZINCFINGER.  
 DR SMART; SM00355; ZnF\_C2H2; 1.  
 DR PROSITE; PS00028; ZINC\_FINGER\_C2H2\_1; 1.  
 DR PROSITE; PS50157; ZINC\_FINGER\_C2H2\_2; 2.  
 KW Metal-binding; Nuclear protein; Zinc; Zinc-finger.  
 FT NON\_TER 1 1  
 FT NON\_TER 53 53  
 SQ SEQUENCE 53 AA; 6029 MW; 783F4B143C4AD012 CRC64;

Query Match 100.0%; Score 30; DB 4; Length 53;  
 Best Local Similarity 100.0%; Pred. No. 15;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQRVH 5  
 |||||  
 Db 6 HQRVH 10

# RESULT 3

O88233

ID O88233 PRELIMINARY; PRT; 57 AA.  
 AC O88233;  
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Mszfl6 (Fragment).  
 GN MSZF16.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL6;  
 RX MEDLINE=98296253; PubMed=9630514;  
 RA Agata Y., Matsuda E., Shimizu A.;  
 RT "Rapid and efficient cloning of cDNAs encoding Krueppel-like zinc  
 RT finger proteins by degenerate PCR."  
 RL Gene 213:55-64(1998).  
 DR EMBL; AB010330; BAA31386.1; -.  
 DR InterPro; IPR007087; Znf\_C2H2.  
 DR InterPro; IPR007086; Znf\_C2H2\_sub.  
 DR Pfam; PF00096; zf-C2H2; 2.  
 DR PRINTS; PR00048; ZINCFINGER.  
 DR ProDom; PD0000003; Znf\_C2H2; 2.  
 DR SMART; SM00355; ZnF\_C2H2; 2.  
 DR PROSITE; PS00028; ZINC\_FINGER\_C2H2\_1; 2.  
 DR PROSITE; PS50157; ZINC\_FINGER\_C2H2\_2; 2.  
 KW Metal-binding; Zinc; Zinc-finger.  
 FT NON\_TER 1 1  
 FT NON\_TER 57 57

SQ SEQUENCE 57 AA; 6468 MW; 01E2DD7DA7E99568 CRC64;

Query Match 100.0%; Score 30; DB 11; Length 57;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQRVH 5  
|||||  
Db 50 HQRVH 54

RESULT 4

Q9QWM7

ID Q9QWM7 PRELIMINARY; PRT; 57 AA.  
AC Q9QWM7;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Mszf92 (Fragment).  
GN MSZF92.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL6;  
RX MEDLINE=98296253; PubMed=9630514;  
RA Agata Y., Matsuda E., Shimizu A.;  
RT "Rapid and efficient cloning of cDNAs encoding Krueppel-like zinc  
RT finger proteins by degenerate PCR."  
RL Gene 213:55-64(1998).  
DR EMBL; AB010356; BAA31412.1; -.  
DR HSSP; P08045; 1ZNF.  
DR InterPro; IPR007087; Znf\_C2H2.  
DR InterPro; IPR007086; Znf\_C2H2\_sub.  
DR Pfam; PF00096; zf-C2H2; 2.  
DR PRINTS; PR00048; ZINCFINGER.  
DR ProDom; PD000003; Znf\_C2H2; 2.  
DR SMART; SM00355; ZnF\_C2H2; 2.  
DR PROSITE; PS00028; ZINC\_FINGER\_C2H2\_1; 2.  
DR PROSITE; PS50157; ZINC\_FINGER\_C2H2\_2; 2.  
KW Metal-binding; Zinc; Zinc-finger.  
FT NON\_TER 1 1  
FT NON\_TER 57 57  
SQ SEQUENCE 57 AA; 6789 MW; 88D5E406C437CA1E CRC64;

Query Match 100.0%; Score 30; DB 11; Length 57;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQRVH 5  
|||||  
Db 50 HQRVH 54

RESULT 5

Q9QWN0

ID Q9QWN0 PRELIMINARY; PRT; 57 AA.  
AC Q9QWN0;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Mszf28 (Fragment).  
GN MSZF28.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL6;  
RX MEDLINE=98296253; PubMed=9630514;  
RA Agata Y., Matsuda E., Shimizu A.;  
RT "Rapid and efficient cloning of cDNAs encoding Krueppel-like zinc  
RT finger proteins by degenerate PCR."  
RL Gene 213:55-64(1998).  
DR EMBL; AB010328; BAA31384.1; -.  
DR HSSP; P08047; 1SP2.  
DR InterPro; IPR007087; Znf\_C2H2.  
DR InterPro; IPR007086; Znf\_C2H2\_sub.  
DR Pfam; PF00096; zf-C2H2; 2.  
DR PRINTS; PR00048; ZINCFINGER.  
DR ProDom; PD000003; Znf\_C2H2; 2.  
DR SMART; SM00355; ZnF\_C2H2; 2.  
DR PROSITE; PS00028; ZINC\_FINGER\_C2H2\_1; 2.  
DR PROSITE; PS50157; ZINC\_FINGER\_C2H2\_2; 2.  
KW Metal-binding; Zinc; Zinc-finger.  
FT NON\_TER 1 1  
FT NON\_TER 57 57  
SQ SEQUENCE 57 AA; 6611 MW; D61698C3A649B8F6 CRC64;

Query Match 100.0%; Score 30; DB 11; Length 57;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQRVH 5  
| | | | |  
Db 22 HQRVH 26

RESULT 6

O14886

ID O14886 PRELIMINARY; PRT; 70 AA.  
AC O14886;  
DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Zinc finger protein (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]

RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RA Sun X., Yu L., Wu G., Liu S., Hu P., Zhang M., Jiang Y., Shouyuan S.;  
 RT "Isolation of novel human genes coding zinc finger protein from brain  
 RT tissue - according to the conservativity of zinc finger motif.";  
 RL Sheng Wu Hua Hsueh Yu Sheng Wu Wu Li Hsueh Pao 0:0-0(1997).  
 DR EMBL; AF027141; AAB84020.1; -.  
 DR InterPro; IPR007087; Znf\_C2H2.  
 DR Pfam; PF00096; zf-C2H2; 2.  
 DR ProDom; PD000003; Znf\_C2H2; 1.  
 DR SMART; SM00355; ZnF\_C2H2; 2.  
 DR PROSITE; PS00028; ZINC\_FINGER\_C2H2\_1; 1.  
 DR PROSITE; PS50157; ZINC\_FINGER\_C2H2\_2; 2.  
 KW Metal-binding; Zinc; Zinc-finger.  
 FT NON\_TER 1 1  
 FT NON\_TER 70 70  
 SQ SEQUENCE 70 AA; 8024 MW; BC3163DAD22E1FAB CRC64;

Query Match 100.0%; Score 30; DB 4; Length 70;  
 Best Local Similarity 100.0%; Pred. No. 20;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQRVH 5  
 |||||  
 Db 25 HQRVH 29

# RESULT 7

O14887

ID O14887 PRELIMINARY; PRT; 74 AA.  
 AC O14887;  
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Zinc finger protein (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE OF 1-72 FROM N.A.  
 RC TISSUE=Brain;  
 RA Sun X., Yu L., Wu G., Liu S., Hu P., Zhang M., Jiang Y., Shouyuan S.;  
 RT "Isolation of novel human genes coding zinc finger protein from brain  
 RT tissue - according to the conservativity of zinc finger motif.";  
 RL Sheng Wu Hua Hsueh Yu Sheng Wu Wu Li Hsueh Pao 0:0-0(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RA Zhang Q.;  
 RL Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AF027142; AAB84021.1; -.  
 DR InterPro; IPR007087; Znf\_C2H2.  
 DR Pfam; PF00096; zf-C2H2; 2.  
 DR ProDom; PD000003; Znf\_C2H2; 2.  
 DR SMART; SM00355; ZnF\_C2H2; 2.  
 DR PROSITE; PS00028; ZINC\_FINGER\_C2H2\_1; 2.

DR PROSITE; PS50157; ZINC\_FINGER\_C2H2\_2; 2.  
KW Metal-binding; Zinc; Zinc-finger.  
FT NON\_TER 1 1  
FT NON\_TER 74 74  
SQ SEQUENCE 74 AA; 8452 MW; FD75F15BDD635243 CRC64;

Query Match 100.0%; Score 30; DB 4; Length 74;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQRVH 5  
|||||  
Db 29 HQRVH 33

RESULT 8

O14888

ID O14888 PRELIMINARY; PRT; 74 AA.  
AC O14888;  
DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Zinc finger protein (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE OF 1-72 FROM N.A.  
RC TISSUE=Brain;  
RA Sun X., Yu L., Wu G., Liu S., Hu P., Zhang M., Jiang Y., Shouyuan S.;  
RT "Isolation of novel human genes coding zinc finger protein from brain  
RT tissue - according to the conservativity of zinc finger motif.";  
RL Sheng Wu Hua Hsueh Yu Sheng Wu Wu Li Hsueh Pao 0:0-0(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RA Zhang Q.;  
RL Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AF027143; AAB84022.1; -.  
DR InterPro; IPR007087; Znf\_C2H2.  
DR Pfam; PF00096; zf-C2H2; 2.  
DR ProDom; PD000003; Znf\_C2H2; 2.  
DR SMART; SM00355; Znf\_C2H2; 2.  
DR PROSITE; PS00028; ZINC\_FINGER\_C2H2\_1; 2.  
DR PROSITE; PS50157; ZINC\_FINGER\_C2H2\_2; 2.  
KW Metal-binding; Zinc; Zinc-finger.  
FT NON\_TER 1 1  
FT NON\_TER 74 74  
SQ SEQUENCE 74 AA; 8564 MW; 6F8711436CC847B6 CRC64;

Query Match 100.0%; Score 30; DB 4; Length 74;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQRVH 5  
|||||

## RESULT 9

O14890

ID O14890 PRELIMINARY; PRT; 75 AA.  
 AC O14890;  
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Zinc finger protein (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE OF 1-72 FROM N.A.  
 RC TISSUE=Brain;  
 RA Sun X., Yu L., Wu G., Liu S., Hu P., Zhang M., Jiang Y., Shouyuan S.;  
 RT "Isolation of novel human genes coding zinc finger protein from brain  
 RT tissue - according to the conservativity of zinc finger motif."  
 RL Sheng Wu Hua Hsueh Yu Sheng Wu Wu Li Hsueh Pao 0:0-0(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RA Zhang Q.;  
 RL Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AF027145; AAB84024.1; -.  
 DR InterPro; IPR007087; Znf\_C2H2.  
 DR InterPro; IPR007086; Znf\_C2H2\_sub.  
 DR Pfam; PF00096; zf-C2H2; 2.  
 DR PRINTS; PR00048; ZINCFINGER.  
 DR ProDom; PD000003; Znf\_C2H2; 2.  
 DR SMART; SM00355; ZnF\_C2H2; 2.  
 DR PROSITE; PS00028; ZINC\_FINGER\_C2H2\_1; 2.  
 DR PROSITE; PS50157; ZINC\_FINGER\_C2H2\_2; 2.  
 KW Metal-binding; Zinc; Zinc-finger.  
 FT NON\_TER 1 1  
 FT NON\_TER 75 75  
 SQ SEQUENCE 75 AA; 8377 MW; 762646DE0AC4E752 CRC64;

Query Match 100.0%; Score 30; DB 4; Length 75;

Best Local Similarity 100.0%; Pred. No. 21;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HQRVH 5

|||||

Db 30 HQRVH 34

## RESULT 10

O88258

ID O88258 PRELIMINARY; PRT; 85 AA.  
 AC O88258;  
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Mszf51 (Fragment).  
 GN MSZF51.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL6;  
 RX MEDLINE=98296253; PubMed=9630514;  
 RA Agata Y., Matsuda E., Shimizu A.;  
 RT "Rapid and efficient cloning of cDNAs encoding Krueppel-like zinc  
 RT finger proteins by degenerate PCR.";  
 RL Gene 213:55-64(1998).  
 DR EMBL; AB010363; BAA31419.1; -.  
 DR InterPro; IPR007087; Znf\_C2H2.  
 DR InterPro; IPR007086; Znf\_C2H2\_sub.  
 DR Pfam; PF00096; zf-C2H2; 3.  
 DR PRINTS; PR00048; ZINCFINGER.  
 DR SMART; SM00355; ZnF\_C2H2; 3.  
 DR PROSITE; PS00028; ZINC\_FINGER\_C2H2\_1; 3.  
 DR PROSITE; PS50157; ZINC\_FINGER\_C2H2\_2; 3.  
 KW Metal-binding; Zinc; Zinc-finger.  
 FT NON\_TER 1 1  
 FT NON\_TER 85 85  
 SQ SEQUENCE 85 AA; 9681 MW; CD65F331C63F5887 CRC64;

Query Match 100.0%; Score 30; DB 11; Length 85;  
 Best Local Similarity 100.0%; Pred. No. 24;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQRVH 5  
 |||||  
 Db 50 HQRVH 54

RESULT 11  
 O88253

ID O88253 PRELIMINARY; PRT; 85 AA.  
 AC O88253;  
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Mszf39 (Fragment).  
 GN ZFP51 OR MSZF39.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL6;  
 RX MEDLINE=98296253; PubMed=9630514;  
 RA Agata Y., Matsuda E., Shimizu A.;  
 RT "Rapid and efficient cloning of cDNAs encoding Krueppel-like zinc  
 RT finger proteins by degenerate PCR.";  
 RL Gene 213:55-64(1998).

DR EMBL; AB010357; BAA31413.1; -.  
 DR HSSP; P08045; 1ZNF.  
 DR MGD; MGI:99198; Zfp51.  
 DR InterPro; IPR007087; Znf\_C2H2.  
 DR InterPro; IPR007086; Znf\_C2H2\_sub.  
 DR Pfam; PF00096; zf-C2H2; 3.  
 DR PRINTS; PR00048; ZINCFINGER.  
 DR ProDom; PD000003; Znf\_C2H2; 3.  
 DR SMART; SM00355; ZnF\_C2H2; 3.  
 DR PROSITE; PS00028; ZINC\_FINGER\_C2H2\_1; 3.  
 DR PROSITE; PS50157; ZINC\_FINGER\_C2H2\_2; 3.  
 KW Metal-binding; Zinc; Zinc-finger.  
 FT NON\_TER 1 1  
 FT NON\_TER 85 85  
 SQ SEQUENCE 85 AA; 10129 MW; 5CE07A6F82393A1A CRC64;

Query Match 100.0%; Score 30; DB 11; Length 85;  
 Best Local Similarity 100.0%; Pred. No. 24;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQRVH 5  
 |||||  
 Db 50 HQRVH 54

# RESULT 12

Q15922

ID Q15922 PRELIMINARY; PRT; 88 AA.  
 AC Q15922;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE DNA-binding protein (Fragment).  
 GN ZNF.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Placenta;  
 RX MEDLINE=92052132; PubMed=1946370;  
 RA Bray P., Lichter P., Thiesen H.J., Ward D.C., Dawid I.B.;  
 RT "Characterization and mapping of human genes encoding zinc finger  
 RT proteins.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 88:9563-9567(1991).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Placenta;  
 RX MEDLINE=92372070; PubMed=1505991;  
 RA Lichter P., Bray P., Ried T., Dawid I.B., Ward D.C.;  
 RT "Clustering of C2-H2 zinc finger motif sequences within telomeric and  
 RT fragile site regions of human chromosomes.";  
 RL Genomics 13:999-1007(1992).  
 CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
 DR EMBL; M88360; AAA61318.1; -.  
 DR PIR; D43284; D43284.



DR HSSP; P08045; 1ZNF.  
 DR GO; GO:0005634; C:nucleus; IEA.  
 DR GO; GO:0003677; F:DNA binding; IEA.  
 DR InterPro; IPR007087; Znf\_C2H2.  
 DR InterPro; IPR007086; Znf\_C2H2\_sub.  
 DR Pfam; PF00096; zf-C2H2; 3.  
 DR PRINTS; PR00048; ZINCFINGER.  
 DR ProDom; PD000003; Znf\_C2H2; 1.  
 DR SMART; SM00355; ZnF\_C2H2; 3.  
 DR PROSITE; PS00028; ZINC\_FINGER\_C2H2\_1; 2.  
 DR PROSITE; PS50157; ZINC\_FINGER\_C2H2\_2; 3.  
 KW DNA-binding; Metal-binding; Nuclear protein; Zinc; Zinc-finger.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 88 AA; 10007 MW; 3C5A45BEA464760E CRC64;

Query Match 100.0%; Score 30; DB 4; Length 88;  
 Best Local Similarity 100.0%; Pred. No. 25;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQRVH 5  
 |||||  
 Db 1 HQRVH 5

# RESULT 13

Q8C2B8

ID Q8C2B8 PRELIMINARY; PRT; 92 AA.  
 AC Q8C2B8;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Zinc finger protein 191 (Fragment).  
 GN ZFP191.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NOD; TISSUE=Thymus;  
 RX MEDLINE=22354683; PubMed=12466851;  
 RA The FANTOM Consortium,  
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs."  
 RL Nature 420:563-573(2002).  
 DR EMBL; AK088914; BAC40649.1; -.  
 DR MGD; MGI:1929704; Zfp191.  
 DR InterPro; IPR007087; Znf\_C2H2.  
 DR InterPro; IPR007086; Znf\_C2H2\_sub.  
 DR Pfam; PF00096; zf-C2H2; 3.  
 DR PRINTS; PR00048; ZINCFINGER.  
 DR ProDom; PD000003; Znf\_C2H2; 3.  
 DR SMART; SM00355; ZnF\_C2H2; 3.  
 DR PROSITE; PS00028; ZINC\_FINGER\_C2H2\_1; 3.  
 DR PROSITE; PS50157; ZINC\_FINGER\_C2H2\_2; 3.  
 FT NON\_TER 1 1

SQ SEQUENCE 92 AA; 10489 MW; 072D7B0903E1C9D3 CRC64;

Query Match 100.0%; Score 30; DB 11; Length 92;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQRVH 5  
|||||  
Db 21 HQRVH 25

RESULT 14

O14899

ID O14899 PRELIMINARY; PRT; 102 AA.  
AC O14899;  
DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Zinc finger protein (ZFP93) (Fragment).  
GN HZF6 OR ZFP93.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98234550; PubMed=9570955;  
RA Shannon M., Stubbs L.;  
RT "Analysis of homologous XRCC1-linked zinc-finger gene families in  
human and mouse: evidence for orthologous genes.";  
RL Genomics 49:112-121(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Kodoyianni V., Ge Y., Krummel G.K., Kvikstad E., Grable L.,  
RA Severin J., Gordon L., Shannon M., Brower A., Olsen A.S., Smith L.M.;  
RT "Sequence analysis of a 1Mb region in 19q13.2 containing a zinc finger  
gene cluster.";  
RL Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.  
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
DR EMBL; AF027514; AAD12729.1; -.  
DR EMBL; AC084239; AAG23969.1; -.  
DR HSSP; P08046; 1AII.  
DR GO; GO:0005634; C:nucleus; IEA.  
DR InterPro; IPR007087; Znf\_C2H2.  
DR InterPro; IPR007086; Znf\_C2H2\_sub.  
DR Pfam; PF00096; zf-C2H2; 3.  
DR PRINTS; PR00048; ZINCFINGER.  
DR ProDom; PD000003; Znf\_C2H2; 2.  
DR SMART; SM00355; ZnF\_C2H2; 3.  
DR PROSITE; PS00028; ZINC\_FINGER\_C2H2\_1; 3.  
DR PROSITE; PS50157; ZINC\_FINGER\_C2H2\_2; 4.  
KW Metal-binding; Nuclear protein; Zinc; Zinc-finger.  
FT NON TER 1 1  
SQ SEQUENCE 102 AA; 11632 MW; 966B8169608186DF CRC64;

Query Match 100.0%; Score 30; DB 4; Length 102;  
Best Local Similarity 100.0%; Pred. No. 29;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQRVH 5  
|||||  
Db 37 HQRVH 41

RESULT 15

Q9UFH1

ID Q9UFH1 PRELIMINARY; PRT; 106 AA.  
AC Q9UFH1;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Hypothetical protein (Fragment).  
GN DKFZP434J0650.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Testis;  
RA Poustka A., Klein M., Mewes H.W., Gassenhuber J., Wiemann S.;  
RL Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.  
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
DR EMBL; AL122078; CAB59253.1; -.  
DR PIR; T34560; T34560.  
DR GO; GO:0005634; C:nucleus; IEA.  
DR InterPro; IPR007087; Znf\_C2H2.  
DR InterPro; IPR007086; Znf\_C2H2\_sub.  
DR Pfam; PF00096; zf-C2H2; 3.  
DR PRINTS; PR00048; ZINCFINGER.  
DR ProDom; PD0000003; Znf\_C2H2; 2.  
DR SMART; SM00355; Znf\_C2H2; 3.  
DR PROSITE; PS00028; ZINC\_FINGER\_C2H2\_1; 2.  
DR PROSITE; PS50157; ZINC\_FINGER\_C2H2\_2; 3.  
KW Hypothetical protein; Metal-binding; Nuclear protein; Zinc;  
KW Zinc-finger.  
FT NON\_TER 1 1  
SQ SEQUENCE 106 AA; 12095 MW; 3D448E0C94F5F16B CRC64;

Query Match 100.0%; Score 30; DB 4; Length 106;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQRVH 5  
|||||  
Db 44 HQRVH 48

Search completed: March 5, 2004, 16:27:29  
Job time : 4.3179 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 5, 2004, 16:15:14 ; Search time 0.679012 Seconds  
(without alignments)  
383.426 Million cell updates/sec

Title: US-10-057-890A-7  
Perfect score: 30  
Sequence: 1 HQRVH 5

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
	1	30	100.0	56	1	ZK23_HUMAN	P17034 homo sapien
	2	30	100.0	56	1	ZN17_HUMAN	P17021 homo sapien
	3	30	100.0	56	1	ZN26_HUMAN	P17031 homo sapien
	4	30	100.0	56	1	ZN29_HUMAN	P17037 homo sapien
	5	30	100.0	87	1	Z154_HUMAN	Q13106 homo sapien
	6	30	100.0	105	1	ZF41_MOUSE	Q02526 mus musculu
	7	30	100.0	106	1	HKR2_HUMAN	P10073 homo sapien
	8	30	100.0	137	1	US33_HCMVA	P09697 human cytom
	9	30	100.0	147	1	PRY_HUMAN	O14603 homo sapien
	10	30	100.0	169	1	ZF58_MOUSE	P16372 mus musculu
	11	30	100.0	172	1	ZG5A_XENLA	P18726 xenopus lae
	12	30	100.0	196	1	ZG3_XENLA	P18718 xenopus lae
	13	30	100.0	201	1	Z239_MOUSE	P24399 mus musculu
	14	30	100.0	209	1	Z235_HUMAN	Q14590 homo sapien
	15	30	100.0	223	1	ZG52_XENLA	P18727 xenopus lae
	16	30	100.0	247	1	ZO20_XENLA	P18744 xenopus lae
	17	30	100.0	301	1	Z11A_HUMAN	P17013 homo sapien

18	30	100.0	348	1	Z134_HUMAN	P52741	homo sapien
19	30	100.0	367	1	Z211_HUMAN	Q13398	homo sapien
20	30	100.0	368	1	ZN24_HUMAN	P17028	homo sapien
21	30	100.0	368	1	ZN24_MOUSE	Q91vn1	mus musculu
22	30	100.0	376	1	GLI4_HUMAN	P10075	homo sapien
23	30	100.0	379	1	Z11B_HUMAN	Q06732	homo sapien
24	30	100.0	393	1	ZF46_MOUSE	Q03309	mus musculu
25	30	100.0	417	1	Z232_HUMAN	Q9uny5	homo sapien
26	30	100.0	420	1	Z229_HUMAN	Q9ujw7	homo sapien
27	30	100.0	445	1	ZG5_XENLA	P18725	xenopus lae
28	30	100.0	451	1	Z222_HUMAN	Q9uk12	homo sapien
29	30	100.0	458	1	Z239_HUMAN	Q16600	homo sapien
30	30	100.0	458	1	Z275_HUMAN	Q9nsd4	homo sapien
31	30	100.0	470	1	Z436_HUMAN	Q9c0f3	homo sapien
32	30	100.0	473	1	ZF38_HUMAN	Q9y5a6	homo sapien
33	30	100.0	474	1	Z230_HUMAN	Q9uie0	homo sapien
34	30	100.0	474	1	Z256_HUMAN	Q9y2p7	homo sapien
35	30	100.0	482	1	Z223_HUMAN	Q9uk11	homo sapien
36	30	100.0	488	1	ZF92_MOUSE	Q62396	mus musculu
37	30	100.0	489	1	ZN71_HUMAN	Q9nqz8	homo sapien
38	30	100.0	498	1	Z271_HUMAN	Q14591	homo sapien
39	30	100.0	510	1	ZF64_HUMAN	P15622	homo sapien
40	30	100.0	518	1	SSG1_Avesa	P12615	avena sativ
41	30	100.0	518	1	SSG2_Avesa	P14812	avena sativ
42	30	100.0	521	1	Z286_HUMAN	Q9hbt8	homo sapien
43	30	100.0	534	1	Z397_HUMAN	Q8nf99	homo sapien
44	30	100.0	536	1	Y628_HUMAN	O75123	homo sapien
45	30	100.0	538	1	Z155_HUMAN	Q12901	homo sapien

# ALIGNMENTS

## RESULT 1

ZK23\_HUMAN

ID ZK23\_HUMAN STANDARD; PRT; 56 AA.

AC P17034;

DT 01-AUG-1990 (Rel. 15, Created)

DT 01-AUG-1990 (Rel. 15, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Zinc finger protein KOX23 (Fragment).

GN KOX23.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Lymphoid;

RX MEDLINE=91145339; PubMed=2288909;

RA Thiesen H.-J.;

RT "Multiple genes encoding zinc finger domains are expressed in human T cells.";

RL New Biol. 2:363-374(1990).

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CC -----

DR EMBL; X52354; CAA36580.1; -.  
DR PIR; I37963; I37963.  
DR InterPro; IPR007087; Znf\_C2H2.  
DR InterPro; IPR007086; Znf\_C2H2\_sub.  
DR Pfam; PF00096; zf-C2H2; 2.  
DR PRINTS; PR00048; ZINCFINGER.  
DR ProDom; PD000003; Znf\_C2H2; 2.  
DR SMART; SM00355; ZnF\_C2H2; 2.  
DR PROSITE; PS00028; ZINC\_FINGER\_C2H2\_1; 2.  
DR PROSITE; PS50157; ZINC\_FINGER\_C2H2\_2; 2.  
KW Zinc-finger; Metal-binding; DNA-binding.  
FT NON\_TER 1 1  
FT ZN\_FING 1 23 C2H2-TYPE.  
FT ZN\_FING 29 51 C2H2-TYPE.  
FT NON\_TER 56 56  
SQ SEQUENCE 56 AA; 6479 MW; B6BC3DEEB62D48CF CRC64;

Query Match 100.0%; Score 30; DB 1; Length 56;  
Best Local Similarity 100.0%; Pred. No. 2.3;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQRVH 5  
| | | | |  
Db 47 HQRVH 51

#### RESULT 2

##### ZN17\_HUMAN

ID ZN17\_HUMAN STANDARD; PRT; 56 AA.  
AC P17021;  
DT 01-AUG-1990 (Rel. 15, Created)  
DT 01-AUG-1990 (Rel. 15, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Zinc finger protein 17 (Zinc finger protein KOX10) (HPF3) (Fragment).  
GN ZNF17 OR KOX10.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lymphoid;  
RX MEDLINE=91145339; PubMed=2288909;  
RA Thiesen H.-J.;  
RT "Multiple genes encoding zinc finger domains are expressed in human T  
RT cells."  
RL New Biol. 2:363-374(1990).  
CC -!- FUNCTION: May function as a transcription factor.  
CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).  
CC -!- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-  
CC FINGER PROTEINS.

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 CC -----

DR EMBL; X52341; CAA36567.1; -.  
 DR PIR; I37949; S10398.  
 DR Genew; HGNC:12958; ZNF17.  
 DR InterPro; IPR007087; Znf\_C2H2.  
 DR InterPro; IPR007086; Znf\_C2H2\_sub.  
 DR Pfam; PF00096; zf-C2H2; 2.  
 DR PRINTS; PR00048; ZINCFINGER.  
 DR SMART; SM00355; Znf\_C2H2; 2.  
 DR PROSITE; PS00028; ZINC\_FINGER\_C2H2\_1; 2.  
 DR PROSITE; PS50157; ZINC\_FINGER\_C2H2\_2; 2.  
 KW Transcription regulation; DNA-binding; Zinc-finger; Metal-binding;  
 KW Nuclear protein; Repeat.  
 FT NON\_TER 1 1  
 FT ZN\_FING 1 23 C2H2-TYPE.  
 FT ZN\_FING 29 51 C2H2-TYPE.  
 FT NON\_TER 56 56  
 SQ SEQUENCE 56 AA; 6704 MW; CD18EF52E08F000C CRC64;

Query Match 100.0%; Score 30; DB 1; Length 56;  
 Best Local Similarity 100.0%; Pred. No. 2.3;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQRVH 5  
 |||||  
 Db 19 HQRVH 23

# RESULT 3

## ZN26\_HUMAN

ID ZN26\_HUMAN STANDARD; PRT; 56 AA.  
 AC P17031;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Zinc finger protein 26 (Zinc finger protein KOX20) (Fragment).  
 GN ZNF26 OR KOX20.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lymphoid;  
 RX MEDLINE=91145339; PubMed=2288909;  
 RA Thiesen H.-J.;  
 RT "Multiple genes encoding zinc finger domains are expressed in human T  
 RT cells."  
 RL New Biol. 2:363-374(1990).

CC -!- FUNCTION: May be involved in transcriptional regulation.  
 CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).  
 CC -!- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-  
 CC FINGER PROTEINS.

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 CC -----

DR EMBL; X52351; CAA36577.1; -.  
 DR PIR; I37960; I37960.  
 DR HSSP; P08045; 1ZNF.  
 DR Genew; HGNC:13053; ZNF26.  
 DR MIM; 194537; -.  
 DR InterPro; IPR007087; Znf\_C2H2.  
 DR InterPro; IPR007086; Znf\_C2H2\_sub.  
 DR Pfam; PF00096; zf-C2H2; 2.  
 DR PRINTS; PR00048; ZINCFINGER.  
 DR ProDom; PD000003; Znf\_C2H2; 2.  
 DR SMART; SM00355; ZnF\_C2H2; 2.  
 DR PROSITE; PS00028; ZINC\_FINGER\_C2H2\_1; 2.  
 DR PROSITE; PS50157; ZINC\_FINGER\_C2H2\_2; 2.  
 KW Transcription regulation; Zinc-finger; DNA-binding; Metal-binding;  
 KW Nuclear protein; Repeat.  
 FT NON\_TER 1 1  
 FT ZN\_FING 1 23 C2H2-TYPE.  
 FT ZN\_FING 29 51 C2H2-TYPE.  
 FT NON\_TER 56 56  
 SQ SEQUENCE 56 AA; 6408 MW; 31ACBC52BBF2855F CRC64;

Query Match 100.0%; Score 30; DB 1; Length 56;  
 Best Local Similarity 100.0%; Pred. No. 2.3;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQRVH 5  
 |||||  
 Db 47 HQRVH 51

#### RESULT 4

ZN29\_HUMAN

ID ZN29\_HUMAN STANDARD; PRT; 56 AA.  
 AC P17037;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Zinc finger protein 29 (Zinc finger protein KOX26) (Fragment).  
 GN ZNF29 OR KOX26.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]



RP SEQUENCE FROM N.A.  
 RC TISSUE=Lymphoid;  
 RX MEDLINE=91145339; PubMed=2288909;  
 RA Thiesen H.-J.;  
 RT "Multiple genes encoding zinc finger domains are expressed in human T  
 RT cells.";  
 RL New Biol. 2:363-374(1990).  
 CC -!- FUNCTION: May be involved in transcriptional regulation.  
 CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).  
 CC -!- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-  
 CC FINGER PROTEINS.

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 CC -----

DR EMBL; X52357; CAA36583.1; -.  
 DR PIR; I37966; I37966.  
 DR Genew; HGNC:13080; ZNF29.  
 DR MIM; 194535; -.  
 DR InterPro; IPR007087; Znf\_C2H2.  
 DR InterPro; IPR007086; Znf\_C2H2\_sub.  
 DR Pfam; PF00096; zf-C2H2; 2.  
 DR PRINTS; PR00048; ZINCFINGER.  
 DR SMART; SM00355; Znf\_C2H2; 2.  
 DR PROSITE; PS00028; ZINC\_FINGER\_C2H2\_1; 1.  
 DR PROSITE; PS50157; ZINC\_FINGER\_C2H2\_2; 2.  
 KW Transcription regulation; Zinc-finger; DNA-binding; Metal-binding;  
 KW Nuclear protein; Repeat.  
 FT NON\_TER 1 1  
 FT ZN\_FING 1 23 C2H2-TYPE.  
 FT ZN\_FING 29 51 C2H2-TYPE.  
 FT NON\_TER 56 56  
 SQ SEQUENCE 56 AA; 6368 MW; D812CCB6BF419884 CRC64;

Query Match 100.0%; Score 30; DB 1; Length 56;  
 Best Local Similarity 100.0%; Pred. No. 2.3;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQRVH 5  
 |||||  
 Db 47 HQRVH 51

RESULT 5  
 Z154\_HUMAN  
 ID Z154 HUMAN STANDARD; PRT; 87 AA.  
 AC Q13106;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Zinc finger protein 154 (Fragment).  
 GN ZNF154.

OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Insulinoma;  
 RX MEDLINE=96044430; PubMed=7557990;  
 RA Tommerup N., Vissing H.;  
 RT "Isolation and fine mapping of 16 novel human zinc finger-encoding  
 RT cDNAs identify putative candidate genes for developmental and  
 RT malignant disorders.";  
 RL Genomics 27:259-264(1995).  
 CC -!- FUNCTION: May be involved in transcriptional regulation.  
 CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).  
 CC -!- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-  
 CC FINGER PROTEINS.  
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 CC -----  
 DR EMBL; U20648; AAC50257.1; -.  
 DR PIR; I38941; I38941.  
 DR HSSP; P08047; 1SP2.  
 DR Genew; HGNC:12939; ZNF154.  
 DR MIM; 604085; -.  
 DR GO; GO:0005634; C:nucleus; NAS.  
 DR GO; GO:0003700; F:transcription factor activity; NAS.  
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; NAS.  
 DR InterPro; IPR007087; Znf\_C2H2.  
 DR InterPro; IPR007086; Znf\_C2H2\_sub.  
 DR Pfam; PF00096; zf-C2H2; 3.  
 DR PRINTS; PR00048; ZINCFINGER.  
 DR SMART; SM00355; ZnF\_C2H2; 3.  
 DR PROSITE; PS00028; ZINC\_FINGER\_C2H2\_1; 3.  
 DR PROSITE; PS50157; ZINC\_FINGER\_C2H2\_2; 3.  
 KW Transcription regulation; DNA-binding; Zinc-finger; Metal-binding;  
 KW Nuclear protein; Repeat.  
 FT NON\_TER 1 1  
 FT ZN\_FING 7 29 C2H2-TYPE.  
 FT ZN\_FING 35 57 C2H2-TYPE.  
 FT ZN\_FING 63 85 C2H2-TYPE.  
 SQ SEQUENCE 87 AA; 10070 MW; 42B9C4E1AC9A92B3 CRC64;

Query Match 100.0%; Score 30; DB 1; Length 87;  
 Best Local Similarity 100.0%; Pred. No. 3.6;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQRVH 5  
 |||||  
 Db 25 HQRVH 29

RESULT 6

ZF41\_MOUSE

ID ZF41\_MOUSE STANDARD; PRT; 105 AA.  
AC Q02526;  
DT 01-OCT-1994 (Rel. 30, Created)  
DT 01-OCT-1994 (Rel. 30, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Zinc finger protein 41 (Zfp-41) (CtFIN92) (Fragment).  
GN ZFP41 OR ZFP-41.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BTBRTF; TISSUE=Spermatocyte;  
RX MEDLINE=93012481; PubMed=1397691;  
RA Noce T., Fujiwara Y., Sezaki M., Fujimoto H., Higashinakagawa T.;  
RT "Expression of a mouse zinc finger protein gene in both spermatocytes  
RT and oocytes during meiosis.";  
RL Dev. Biol. 153:356-367(1992).  
CC -!- FUNCTION: A PUTATIVE DNA-BINDING REGULATORY PROTEIN ASSOCIATED  
CC WITH MEIOSIS IN SPERMATOGENESIS.  
CC -!- SUBCELLULAR LOCATION: Nuclear.  
CC -!- TISSUE SPECIFICITY: PREDOMINANTLY IN THE SPERMATOCYTES AND  
CC SPERMATIDS OF TESTES. IT IS ALSO EXPRESSED IN THE FETUS AND  
CC EMBRYONIC STEM CELLS AT LOWER LEVELS.  
CC -!- DEVELOPMENTAL STAGE: DETECTED IN THE NEWBORN TESTIS AND PEAKS  
CC AT 3 WEEKS DURING THE FIRST CYCLE OF SPERMATOGENESIS. EXPRESSED  
CC IN THE FETUS AND EMBRYO.  
CC -!- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-  
CC FINGER PROTEINS.  
CC -----  
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CC -----  
DR EMBL; D10631; BAA01481.1; -.  
DR PIR; B48827; B48827.  
DR HSSP; P08046; 1A1I.  
DR MGD; MGI:99186; Zfp41.  
DR InterPro; IPR007087; Znf\_C2H2.  
DR InterPro; IPR007086; Znf\_C2H2\_sub.  
DR Pfam; PF00096; zf-C2H2; 4.  
DR PRINTS; PR00048; ZINCFINGER.  
DR SMART; SM00355; ZnF\_C2H2; 4.  
DR PROSITE; PS00028; ZINC\_FINGER\_C2H2\_1; 4.  
DR PROSITE; PS50157; ZINC\_FINGER\_C2H2\_2; 4.  
KW Zinc-finger; Metal-binding; Developmental protein; Spermatogenesis;  
KW Nuclear protein; Transcription regulation; DNA-binding; Repeat.  
FT NON\_TER 1 1  
FT ZN\_FING 1 20 C2H2-TYPE.

FT ZN\_FING 29 49 C2H2-TYPE.  
 FT ZN\_FING 57 76 C2H2-TYPE.  
 FT ZN\_FING 85 105 C2H2-TYPE.  
 FT NON\_TER 105 105  
 SQ SEQUENCE 105 AA; 12083 MW; 2A29456BB9A74B1F CRC64;

Query Match 100.0%; Score 30; DB 1; Length 105;  
 Best Local Similarity 100.0%; Pred. No. 4.4;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HQRVH 5  
 |||||  
 Db 17 HQRVH 21

# RESULT 7

## HKR2\_HUMAN

ID HKR2\_HUMAN STANDARD; PRT; 106 AA.  
 AC P10073;  
 DT 01-MAR-1989 (Rel. 10, Created)  
 DT 01-MAR-1989 (Rel. 10, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Krueppel-related zinc finger protein 2 (HKR2 protein) (Fragment).  
 GN HKR2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89096896; PubMed=2850480;  
 RA Ruppert J.M., Kinzler K.W., Wong A.J., Bigner S.H., Kao F.T.,  
 RA Law M.L., Seuanez H.N., O'Brien S.J., Vogelstein B.;  
 RT "The GLI-Kruppel family of human genes."  
 RL Mol. Cell. Biol. 8:3104-3113(1988).  
 CC -!- FUNCTION: May be involved in transcriptional regulation.  
 CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).  
 CC -!- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-  
 CC FINGER PROTEINS.  
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 CC -----  
 DR EMBL; M20676; -; NOT\_ANNOTATED\_CDS.  
 DR PIR; D31201; D31201.  
 DR HSSP; P08045; 1ZNF.  
 DR Genew; HGNC:4929; HKR2.  
 DR MIM; 165260; -.  
 DR GO; GO:0005634; C:nucleus; NAS.  
 DR InterPro; IPR007087; Znf\_C2H2.  
 DR InterPro; IPR007086; Znf\_C2H2\_sub.  
 DR Pfam; PF00096; zf-C2H2; 3.

DR PRINTS; PR00048; ZINCFINGER.  
 DR SMART; SM00355; ZnF\_C2H2; 3.  
 DR PROSITE; PS00028; ZINC\_FINGER\_C2H2\_1; 2.  
 DR PROSITE; PS50157; ZINC\_FINGER\_C2H2\_2; 4.  
 KW Transcription regulation; DNA-binding; Zinc-finger; Metal-binding;  
 KW Nuclear protein; Repeat.  
 FT NON\_TER 1 1  
 FT ZN\_FING 7 25 C2H2-TYPE.  
 FT ZN\_FING 31 54 C2H2-TYPE.  
 FT ZN\_FING 59 82 C2H2-TYPE.  
 FT ZN\_FING 87 >106 C2H2-TYPE.  
 FT NON\_TER 106 106  
 SQ SEQUENCE 106 AA; 12068 MW; 95A57A8EA865B403 CRC64;

Query Match 100.0%; Score 30; DB 1; Length 106;  
 Best Local Similarity 100.0%; Pred. No. 4.4;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQRVH 5  
 |||||  
 Db 77 HQRVH 81

# RESULT 8

US33\_HCMVA

ID US33\_HCMVA STANDARD; PRT; 137 AA.  
 AC P09697;  
 DT 01-MAR-1989 (Rel. 10, Created)  
 DT 01-MAR-1989 (Rel. 10, Last sequence update)  
 DT 01-FEB-1991 (Rel. 17, Last annotation update)  
 DE Hypothetical protein HHLF3.  
 GN US33.  
 OS Human cytomegalovirus (strain AD169).  
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
 OC Betaherpesvirinae; Cytomegalovirus.  
 OX NCBI\_TaxID=10360;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87169717; PubMed=3031311;  
 RA Weston K., Barrell B.G.;  
 RT "Sequence of the short unique region, short repeats, and part of the  
 RT long repeats of human cytomegalovirus."  
 RL J. Mol. Biol. 192:177-208(1986).  
 RN [2]  
 RP COMPLETE GENOME.  
 RX MEDLINE=90269039; PubMed=2161319;  
 RA Chee M.S., Bankier A.T., Beck S., Bohni R., Brown C.M., Cerny R.,  
 RA Horsnell T., Hutchison C.A. III, Kouzarides T., Martignetti J.A.,  
 RA Preddie E., Satchwell S.C., Tomlinson P., Weston K.M., Barrell B.G.;  
 RT "Analysis of the protein-coding content of the sequence of human  
 RT cytomegalovirus strain AD169."  
 RL Curr. Top. Microbiol. Immunol. 154:125-169(1990).

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CC -----

DR EMBL; X17403; CAA35266.1; -.  
DR EMBL; X04650; CAB37119.1; -.  
DR PIR; I27216; QQBED9.  
KW Hypothetical protein.  
SQ SEQUENCE 137 AA; 15774 MW; 17DE2F61C2A859B5 CRC64;

Query Match 100.0%; Score 30; DB 1; Length 137;  
Best Local Similarity 100.0%; Pred. No. 5.8;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQRVH 5  
|||||  
Db 72 HQRVH 76

#### RESULT 9

##### PRY\_HUMAN

ID PRY\_HUMAN STANDARD; PRT; 147 AA.  
AC O14603;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE PTPN13-like protein, Y-linked (Testis-specific PTP-BL related Y  
DE protein).  
GN PRY OR PTPN13LY.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RC TISSUE=Testis;  
RX MEDLINE=98022381; PubMed=9381176;  
RA Lahn B.T., Page D.C.;  
RT "Functional coherence of the human Y chromosome.";  
RL Science 278:675-680(1997).  
RN [2]  
RP REVISION.  
RA Lahn B.T., Page D.C.;  
RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORM 2).  
RX MEDLINE=22699787; PubMed=12815422;  
RA Skaletsky H., Kuroda-Kawaguchi T., Minx P.J., Cordum H.S.,  
RA Hillier L.W., Brown L.G., Repping S., Pyntikova T., Ali J., Bieri T.,  
RA Chinwalla A., Delehaunty A., Delehaunty K., Du H., Fewell G.,  
RA Fulton L., Fulton R., Graves T.A., Hou S.-F., Latrielle P.,  
RA Leonard S., Mardis E., Maupin R., McPherson J., Miner T., Nash W.,  
RA Nguyen C., Ozersky P., Pepin K., Rock S., Rohlffing T., Scott K.,  
RA Schultz B., Strong C., Tin-Wollam A., Yang S.-P., Waterston R.H.,  
RA Wilson R.K., Rozen S., Page D.C.;  
RT "The male-specific region of the human Y chromosome is a mosaic of  
RT discrete sequence classes.";

RL Nature 423:825-837(2003).  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=1;  
 CC IsoId=O14603-1; Sequence=Displayed;  
 CC Name=2;  
 CC IsoId=O14603-2; Sequence=VSP\_004068, VSP\_004069;  
 CC Note=No experimental confirmation available;  
 CC -!- TISSUE SPECIFICITY: Testis.  
 CC -!- CAUTION: PRY has multiple locations on chromosome Y.  
 CC -----  
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 CC -----  
 DR EMBL; AF000988; AAC51835.2; -.  
 DR EMBL; AF517635; AAN06674.1; -.  
 DR Genew; HGNC:14024; PRY.  
 DR MIM; 400019; -.  
 KW Alternative splicing.  
 FT VARSPLIC 63 71 YGKVGCI SL -> DGVSPCLPC (in isoform 2).  
 FT /FTId=VSP\_004068.  
 FT VARSPLIC 72 147 Missing (in isoform 2).  
 FT /FTId=VSP\_004069.  
 SQ SEQUENCE 147 AA; 16512 MW; 87C861FC2BEDAE9B CRC64;  
  
 Query Match 100.0%; Score 30; DB 1; Length 147;  
 Best Local Similarity 100.0%; Pred. No. 6.2;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 1 HQRVH 5  
 |||||  
 Db 93 HQRVH 97

# RESULT 10

ZF58\_MOUSE

ID ZF58\_MOUSE STANDARD; PRT; 169 AA.  
 AC P16372;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Zinc finger protein 58 (Zfp-58) (Zinc finger protein Mfg-1)  
 DE (Fragment).  
 GN ZFP58 OR MFG-1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CD-1; TISSUE=Skeletal muscle;  
 RX MEDLINE=90083278; PubMed=2512579;

```

RA  Passananti C., Felsani A., Caruso M., Amati P.;
RT  "Mouse genes coding for 'zinc-finger'-containing proteins:
RT  characterization and expression in differentiated cells.";
RL  Proc. Natl. Acad. Sci. U.S.A. 86:9417-9421(1989).
CC  -!- FUNCTION: May have a role during differentiation processes.
CC  -!- SUBCELLULAR LOCATION: Nuclear (Probable).
CC  -!- TISSUE SPECIFICITY: Liver; testis; and at considerably lower
CC      levels in brain, spleen and heart.
CC  -!- DEVELOPMENTAL STAGE: Expression is positively regulated upon
CC      differentiation and is not related to the cell cycle.
CC  -!- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-
CC      FINGER PROTEINS.
CC  -----
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CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; M28513; AAA39531.1; -.
DR  PIR; A39240; A39240.
DR  HSSP; P25490; 1UBD.
DR  MGD; MGI:99205; Zfp58.
DR  InterPro; IPR007087; Znf_C2H2.
DR  InterPro; IPR007086; Znf_C2H2_sub.
DR  Pfam; PF00096; zf-C2H2; 6.
DR  PRINTS; PR00048; ZINCFINGER.
DR  SMART; SM00355; ZnF_C2H2; 6.
DR  PROSITE; PS00028; ZINC_FINGER_C2H2_1; 5.
DR  PROSITE; PS50157; ZINC_FINGER_C2H2_2; 6.
KW  Zinc-finger; Metal-binding; DNA-binding; Repeat; Nuclear protein.
FT  NON_TER      1      1
FT  ZN_FING      8      30      C2H2-TYPE.
FT  ZN_FING     36      58      C2H2-TYPE.
FT  ZN_FING     64      86      C2H2-TYPE.
FT  ZN_FING     92     114      C2H2-TYPE.
FT  ZN_FING    120     142      C2H2-TYPE.
FT  ZN_FING    148    >169      C2H2-TYPE.
FT  NON_TER    169     169
SQ  SEQUENCE    169 AA;  19585 MW;  7F55256B1406CDA3 CRC64;

Query Match      100.0%; Score 30; DB 1; Length 169;
Best Local Similarity 100.0%; Pred. No. 7.2;
Matches      5; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

Qy      1 HQRVH 5
        |||||
Db      54 HQRVH 58

RESULT 11
ZG5A_XENLA
ID  ZG5A_XENLA      STANDARD;      PRT;      172 AA.
AC  P18726;
DT  01-NOV-1990 (Rel. 16, Created)

```



DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Gastrula zinc finger protein XLCGF51.1A (Fragment).  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OX NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90040698; PubMed=2509712;  
 RA Nietfeld W., El-Baradi T., Mentzel H., Pieler T., Koester M.,  
 RA Poeting A., Knoechel W.;  
 RT "Second-order repeats in Xenopus laevis finger proteins.";  
 RL J. Mol. Biol. 208:639-659(1989).  
 DR PIR; S06575; S06575.  
 DR HSSP; P03001; 1TF3.  
 DR InterPro; IPR007087; Znf\_C2H2.  
 DR Pfam; PF00096; zf-C2H2; 6.  
 DR SMART; SM00355; ZnF\_C2H2; 6.  
 DR PROSITE; PS00028; ZINC\_FINGER\_C2H2\_1; 6.  
 DR PROSITE; PS00157; ZINC\_FINGER\_C2H2\_2; 6.  
 KW Zinc-finger; Metal-binding; DNA-binding; Repeat.  
 FT NON\_TER 1 1  
 FT ZN\_FING 6 28 C2H2-TYPE.  
 FT ZN\_FING 34 56 C2H2-TYPE.  
 FT ZN\_FING 62 84 C2H2-TYPE.  
 FT ZN\_FING 90 112 C2H2-TYPE.  
 FT ZN\_FING 122 144 C2H2-TYPE.  
 FT ZN\_FING 150 172 C2H2-TYPE.  
 FT NON\_TER 172 172  
 SQ SEQUENCE 172 AA; 19609 MW; AF8290211AB5E0D0 CRC64;

Query Match 100.0%; Score 30; DB 1; Length 172;  
 Best Local Similarity 100.0%; Pred. No. 7.3;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HQRVH 5  
 |||||  
 Db 168 HQRVH 172

# RESULT 12

ZG3\_XENLA

ID ZG3\_XENLA STANDARD; PRT; 196 AA.

AC P18718;

DT 01-NOV-1990 (Rel. 16, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Gastrula zinc finger protein XLCGF3.1 (Fragment).

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;

OC Xenopodinae; Xenopus.

OX NCBI\_TaxID=8355;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=90040698; PubMed=2509712;  
 RA Nietfeld W., El-Baradi T., Mentzel H., Pieler T., Koester M.,  
 RA Poeting A., Knoechel W.;  
 RT "Second-order repeats in *Xenopus laevis* finger proteins.";  
 RL J. Mol. Biol. 208:639-659(1989).  
 DR PIR; S06558; S06558.  
 DR HSSP; P08047; 1SP2.  
 DR InterPro; IPR007087; Znf\_C2H2.  
 DR InterPro; IPR007086; Znf\_C2H2\_sub.  
 DR Pfam; PF00096; zf-C2H2; 7.  
 DR PRINTS; PR00048; ZINCFINGER.  
 DR SMART; SM00355; ZnF\_C2H2; 7.  
 DR PROSITE; PS00028; ZINC\_FINGER\_C2H2\_1; 7.  
 DR PROSITE; PS50157; ZINC\_FINGER\_C2H2\_2; 7.  
 KW Zinc-finger; Metal-binding; DNA-binding; Repeat.  
 FT NON\_TER 1 1  
 FT ZN\_FING 6 28 C2H2-TYPE.  
 FT ZN\_FING 34 56 C2H2-TYPE.  
 FT ZN\_FING 62 84 C2H2-TYPE.  
 FT ZN\_FING 90 112 C2H2-TYPE.  
 FT ZN\_FING 118 140 C2H2-TYPE.  
 FT ZN\_FING 146 168 C2H2-TYPE.  
 FT ZN\_FING 174 196 C2H2-TYPE.  
 FT NON\_TER 196 196  
 SQ SEQUENCE 196 AA; 22378 MW; B5735306E722FFDC CRC64;

Query Match 100.0%; Score 30; DB 1; Length 196;  
 Best Local Similarity 100.0%; Pred. No. 8.4;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQRVH 5  
 |||||  
 Db 136 HQRVH 140

# RESULT 13

## Z239\_MOUSE

ID Z239\_MOUSE STANDARD; PRT; 201 AA.  
 AC P24399;  
 DT 01-MAR-1992 (Rel. 21, Created)  
 DT 01-MAR-1992 (Rel. 21, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Zinc finger protein 239 (Zfp-239) (Zinc finger protein MOK-2).  
 GN ZNF239 OR ZFP239 OR MOK2 OR MOK-2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90097859; PubMed=2104662;  
 RA Ernoult-Lange M., Kress M., Hamer D.;  
 RT "A gene that encodes a protein consisting solely of zinc finger  
 RT domains is preferentially expressed in transformed mouse cells.";  
 RL Mol. Cell. Biol. 10:418-421(1990).  
 CC !- FUNCTION: May function as a transcription factor.  
 CC !- SUBCELLULAR LOCATION: Nuclear (Potential).

CC -!- TISSUE SPECIFICITY: PREFERENTIALLY EXPRESSED IN TRANSFORMED  
 CC MOUSE CELLS.  
 CC -!- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-  
 CC FINGER PROTEINS.  
 CC -!- SIMILARITY: Contains 7 C2H2-type zinc fingers.  
 CC -----  
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 CC -----  
 DR EMBL; M32057; AAA39729.1; -.  
 DR PIR; I57505; I57505.  
 DR HSSP; P08047; 1SP2.  
 DR TRANSFAC; T00510; -.  
 DR MGD; MGI:1306812; Zfp239.  
 DR InterPro; IPR007087; Znf\_C2H2.  
 DR InterPro; IPR007086; Znf\_C2H2\_sub.  
 DR Pfam; PF00096; zf-C2H2; 7.  
 DR PRINTS; PR00048; ZINCFINGER.  
 DR ProDom; PD000003; Znf\_C2H2; 6.  
 DR SMART; SM00355; ZnF\_C2H2; 7.  
 DR PROSITE; PS00028; ZINC\_FINGER\_C2H2\_1; 7.  
 DR PROSITE; PS50157; ZINC\_FINGER\_C2H2\_2; 7.  
 KW Transcription regulation; DNA-binding; Zinc-finger; Metal-binding;  
 KW Nuclear protein; Repeat.  
 FT ZN\_FING 6 28 C2H2-TYPE 1.  
 FT ZN\_FING 34 56 C2H2-TYPE 2.  
 FT ZN\_FING 62 84 C2H2-TYPE 3.  
 FT ZN\_FING 90 112 C2H2-TYPE 4.  
 FT ZN\_FING 118 140 C2H2-TYPE 5.  
 FT ZN\_FING 146 168 C2H2-TYPE 6.  
 FT ZN\_FING 174 196 C2H2-TYPE 7.  
 SQ SEQUENCE 201 AA; 22832 MW; B7A18C0AADAB1384 CRC64;

Query Match 100.0%; Score 30; DB 1; Length 201;  
 Best Local Similarity 100.0%; Pred. No. 8.6;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQRVH 5  
 |||||  
 Db 80 HQRVH 84

#### RESULT 14

Z235\_HUMAN

ID Z235\_HUMAN STANDARD; PRT; 209 AA.  
 AC Q14590;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Zinc finger protein 235 (Zinc finger protein 93'homolog) (Zfp-93)  
 DE (Zinc finger protein HZF6) (Fragment).  
 GN ZNF235 OR ZFP93 OR ZNF270.

OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95169271; PubMed=7865130;  
 RA Abrink M., Aveskogh M., Hellman L.;  
 RT "Isolation of cDNA clones for 42 different Kruppel-related zinc finger  
 RT proteins expressed in the human monoblast cell line U-937.";  
 RL DNA Cell Biol. 14:125-136(1995).  
 CC -!- FUNCTION: May function as a transcription factor.  
 CC -!- SUBCELLULAR LOCATION: Nuclear (Probable).  
 CC -!- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-  
 CC FINGER PROTEINS.

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 CC -----

DR EMBL; X78929; CAA55529.1; -.  
 DR PIR; S47068; S47068.  
 DR HSSP; P25490; 1ZNM.  
 DR Genew; HGNC:12866; ZNF235.  
 DR MIM; 604749; -.  
 DR InterPro; IPR007087; Znf\_C2H2.  
 DR InterPro; IPR007086; Znf\_C2H2\_sub.  
 DR Pfam; PF00096; zf-C2H2; 7.  
 DR PRINTS; PR00048; ZINCFINGER.  
 DR ProDom; PD000003; Znf\_C2H2; 6.  
 DR SMART; SM00355; ZnF\_C2H2; 7.  
 DR PROSITE; PS00028; ZINC\_FINGER\_C2H2\_1; 7.  
 DR PROSITE; PS0157; ZINC\_FINGER\_C2H2\_2; 7.  
 KW Transcription regulation; DNA-binding; Zinc-finger; Metal-binding;  
 KW Nuclear protein; Repeat.  
 FT NON\_TER 1 1  
 FT ZN\_FING 4 26 C2H2-TYPE.  
 FT ZN\_FING 32 54 C2H2-TYPE.  
 FT ZN\_FING 60 82 C2H2-TYPE.  
 FT ZN\_FING 88 110 C2H2-TYPE.  
 FT ZN\_FING 116 138 C2H2-TYPE.  
 FT ZN\_FING 144 166 C2H2-TYPE.  
 FT ZN\_FING 172 194 C2H2-TYPE.  
 FT ZN\_FING 200 >209 C2H2-TYPE.  
 FT NON\_TER 209 209  
 SQ SEQUENCE 209 AA; 23915 MW; 9C12DE06BC7FFC8E CRC64;

Query Match 100.0%; Score 30; DB 1; Length 209;  
 Best Local Similarity 100.0%; Pred. No. 8.9;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQRVH 5  
 |||||

Db

22 HQRVH 26

## RESULT 15

ZG52\_XENLA

ID ZG52\_XENLA STANDARD; PRT; 223 AA.  
 AC P18727;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Gastrula zinc finger protein XLCGF52.1 (Fragment).  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OX NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90040698; PubMed=2509712;  
 RA Nietfeld W., El-Baradi T., Mentzel H., Pieler T., Koester M.,  
 RA Poeting A., Knoechel W.;  
 RT "Second-order repeats in Xenopus laevis finger proteins.";  
 RL J. Mol. Biol. 208:639-659(1989).  
 DR PIR; S06576; S06576.  
 DR HSSP; P25490; 1UBD.  
 DR InterPro; IPR007087; Znf\_C2H2.  
 DR InterPro; IPR007086; Znf\_C2H2\_sub.  
 DR Pfam; PF00096; zf-C2H2; 8.  
 DR PRINTS; PR00048; ZINCFINGER.  
 DR SMART; SM00355; ZnF\_C2H2; 8.  
 DR PROSITE; PS00028; ZINC\_FINGER\_C2H2\_1; 7.  
 DR PROSITE; PS50157; ZINC\_FINGER\_C2H2\_2; 8.  
 KW Zinc-finger; Metal-binding; DNA-binding; Repeat.  
 FT NON\_TER 1 1  
 FT ZN\_FING 6 27 C2H2-TYPE.  
 FT ZN\_FING 33 55 C2H2-TYPE.  
 FT ZN\_FING 61 83 C2H2-TYPE.  
 FT ZN\_FING 89 111 C2H2-TYPE.  
 FT ZN\_FING 117 139 C2H2-TYPE.  
 FT ZN\_FING 145 167 C2H2-TYPE.  
 FT ZN\_FING 173 195 C2H2-TYPE.  
 FT ZN\_FING 201 223 C2H2-TYPE.  
 FT NON\_TER 223 223  
 SQ SEQUENCE 223 AA; 25549 MW; BFA977BB6701BA96 CRC64;

Query Match 100.0%; Score 30; DB 1; Length 223;

Best Local Similarity 100.0%; Pred. No. 9.6;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQRVH 5

||||

Db 51 HQRVH 55

Search completed: March 5, 2004, 16:23:40

Job time : 0.679012 secs